



CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
SEQUENCE LISTING

- <110> Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
- <130> 10466-14
- <140> 09/665,350
<141> 2000-09-18
- <150> PCT/US00/04414
<151> 2000-02-22
- <150> US 60/143,048
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- <150> US 60/145,698
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- <150> US 60/146,222
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- <150> PCT/US99/20594
<151> 1999-09-08
- <150> PCT/US99/20944
<151> 1999-09-13
- <150> PCT/US99/21090
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- <150> PCT/US99/21547
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- <150> PCT/US99/23089
<151> 1999-10-05

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<150> PCT/US99/28214
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<151> 2000-01-05

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<213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met Val Asp Thr
35 40 45
Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Lys Thr
50 55 60
Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu Leu Glu Ile Leu Glu
65 70 75 80
Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys Asn Gln Met Leu Glu Ala
85 90 95
Gln Glu Glu His Leu Glu Ala Trp Trp Leu Gln Leu Lys Ser Glu Tyr
100 105 110
Pro Asp Leu Phe Glu Trp Phe Cys Val Lys Thr Leu Lys Val Cys Cys
115 120 125
Ser Pro Gly Thr Tyr Gly Pro Asp Cys Leu Ala Cys Gln Gly Gly Ser
130 135 140
Gln Arg Pro Cys Ser Gly Asn Gly His Cys Ser Gly Asp Gly Ser Arg
145 150 155 160
Gln Gly Asp Gly Ser Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu
165 170 175
Cys Thr Asp Cys Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr
180 185 190
His Ser Ile Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly
195 200 205
Leu Thr Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp
210 215 220
Glu Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
225 230 235 240
Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr Cys
245 250 255
Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly Pro Gly
260 265 270
Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His Gly Gln Cys
275 280 285
Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr Cys Val Arg Lys

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290

295

300

Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr Val Cys Val Cys Pro
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Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys Val Pro Pro Ala Glu Ala
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Glu Ala Thr Glu Gly Glu Ser Pro Thr Gln Leu Pro Ser Arg Glu Asp
 340 345 350

Leu

<210> 3

<211> 2206

<212> DNA

<213> Homo sapiens

<400> 3

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| tcgacctcga | cccacgcgtc | cgccaggccg | ggaggcgacg | cgcccagccg | tctaaacggg | 120 |
| aacagccctg | gctgagggag | ctgcagcgca | gcagagtatc | tgacggcgcc | aggttgcgta | 180 |
| ggtgcggcac | gaggagtttt | cccggcagcg | aggaggtcct | gagcagcatg | gcccggagga | 240 |
| gcgccttccc | tgccgccgcg | ctctggctct | ggagcatcct | cctgtgcctg | ctggcactgc | 300 |
| gggcgagggc | cgggccgccc | caggaggaga | gcctgtacct | atggatcgat | gctcaccagg | 360 |
| caagagtact | cataggattt | gaagaagata | tcctgattgt | ttcagagggg | aaaatggcac | 420 |
| cttttacaca | tgatttcaga | aaagcgcaac | agagaatgcc | agctattcct | gtcaatatcc | 480 |
| attccatgaa | ttttacctgg | caagctgcag | ggcaggcaga | atacttctat | gaattcctgt | 540 |
| ccttgcgctc | cctggataaa | ggcatcatgg | cagatccaac | cgtcaatgtc | cctctgctgg | 600 |
| gaacagtgcc | tcacaaggca | tcagttgttc | aagttggttt | cccatgtcct | ggaaaacagg | 660 |
| atgggggtggc | agcatttgaa | gtggatgtga | ttgttatgaa | ttctgaaggc | aacaccattc | 720 |
| tccaaacacc | tcaaaatgct | atcttcttta | aaacatgtca | acaagctgag | tgcccaggcg | 780 |
| ggtgcccga | tggaggcttt | tgtaatgaaa | gacgcatctg | cgagtgtcct | gatgggttcc | 840 |
| acggacctca | ctgtgagaaa | gccctttgta | ccccacgatg | tatgaatggg | ggactttgtg | 900 |
| tgactcctgg | tttctgcatc | tgcccacctg | gattctatgg | agtgaactgt | gacaaagcaa | 960 |
| actgtcaac | cacctgcttt | aatggaggga | cctgtttcta | ccctggaaaa | tgtatttgcc | 1020 |
| ctccaggact | agaggggagag | cagtgtgaaa | tcagcaaattg | cccacaaccc | tgtcgaaatg | 1080 |
| gaggtaaatg | cattggtaaa | agcaaattga | agtgtttcaa | aggttaccag | ggagacctct | 1140 |
| gttcaaaggc | tgtctgcgag | cctggctgtg | gtgcacatgg | aacctgccat | gaacccaaca | 1200 |
| aatgccaatg | tcaagaagggt | tggcatggaa | gacactgcaa | taaaagggtac | gaagccagcc | 1260 |
| tcatacatgc | cctgaggcca | gcaggcgccc | agctcaggca | gcacacgcct | tcacttaaaa | 1320 |
| aggccgagga | gcggcgggat | ccacctgaat | ccaattacat | ctgggtgaact | ccgacatctg | 1380 |
| aaacgtttta | agttacacca | agttcatagc | ctttgttaac | ctttcatgtg | ttgaatgttc | 1440 |
| aaataatggt | cattacactt | aagaatactg | gcctgaattt | tattagcttc | attataaatc | 1500 |
| actgagctga | tatttactct | tccttttaag | ttttctaagt | acgtctgtag | catgatggta | 1560 |
| tagattttct | tgtttcagtg | ctttgggaca | gattttatat | tatgtcaatt | gatcagggtta | 1620 |
| aaattttcag | tgtgtagtgt | gcagatatatt | tcaaaattac | aatgcattta | tgggtgtctgg | 1680 |
| gggcagggga | acatcagaaa | ggttaaattg | ggcaaaaatg | cgtaagtcac | aagaatttgg | 1740 |
| atgggtgcagt | taatgttgaa | gttacagcat | ttcagatttt | attgtcagat | atttagatgt | 1800 |
| ttgttacatt | tttaaaaatt | gctcttaatt | tttaaaactct | caataacaata | tattttgacc | 1860 |
| ttaccattat | tccagagatt | cagtattaaa | aaaaaaaaaa | ttacactgtg | gtagtggcat | 1920 |
| ttaaacaata | taatatattc | taaacacaat | gaaataggga | atataatgta | tgaacttttt | 1980 |
| gcattggctt | gaagcaatat | aatatattgt | aaacaaaaca | cagctcttac | ctaataaaca | 2040 |
| ttttatactg | tttgtatgta | taaaataaag | gtgctgcttt | agttttttgg | aaaaaaaaaa | 2100 |
| aaaaaaaaaa | aaaaaaaaaa | aaaaaaaaaa | gggcggccgc | gactctagag | tcgacctgca | 2160 |
| gaagcttggc | cgccatggcc | caacttgttt | attgcagctt | ataatg | | 2206 |

<210> 4

<211> 379

<212> PRT

<213> Homo sapiens

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<400> 4

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Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala Arg Val Leu
          35          40          45
Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu Gly Lys Met Ala
          50          55          60
Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln Arg Met Pro Ala Ile
          65          70          75          80
Pro Val Asn Ile His Ser Met Asn Phe Thr Trp Gln Ala Ala Gly Gln
          85          90          95
Ala Glu Tyr Phe Tyr Glu Phe Leu Ser Leu Arg Ser Leu Asp Lys Gly
          100          105          110
Ile Met Ala Asp Pro Thr Val Asn Val Pro Leu Leu Gly Thr Val Pro
          115          120          125
His Lys Ala Ser Val Val Gln Val Gly Phe Pro Cys Leu Gly Lys Gln
          130          135          140
Asp Gly Val Ala Ala Phe Glu Val Asp Val Ile Val Met Asn Ser Glu
          145          150          155          160
Gly Asn Thr Ile Leu Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr
          165          170          175
Cys Gln Gln Ala Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys
          180          185          190
Asn Glu Arg Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His
          195          200          205
Cys Glu Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys
          210          215          220
Val Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
          225          230          235          240
Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr Cys
          245          250          255
Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly Glu Gln
          260          265          270
Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly Gly Lys Cys
          275          280          285
Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr Gln Gly Asp Leu
          290          295          300
Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly Ala His Gly Thr Cys
          305          310          315          320
His Glu Pro Asn Lys Cys Gln Cys Gln Glu Gly Trp His Gly Arg His
          325          330          335

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Cys Asn Lys Arg Tyr Glu Ala Ser Leu Ile His Ala Leu Arg Pro Ala
340 345 350

Gly Ala Gln Leu Arg Gln His Thr Pro Ser Leu Lys Lys Ala Glu Glu
355 360 365

Arg Arg Asp Pro Pro Glu Ser Asn Tyr Ile Trp
370 375

<210> 5

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 5

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<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 6

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<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 7

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<210> 8

<211> 49

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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<210> 9

<211> 22

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

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22

<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 10

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23

<210> 11

<211> 2197

<212> DNA

<213> Homo sapiens

<400> 11

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| ggccccagcc | cacaccttca | ccagggccca | ggagccacca | tgtggcgatg | tccactgggg | 120 |
| ctactgctgt | tgctgccgct | ggctggccac | ttggctctgg | gtgccagca | gggtcgtggg | 180 |
| cgccgggagc | tagcaccggg | tctgcacctg | cggggcatcc | gggacgcggg | aggccggtac | 240 |
| tgccaggagc | aggacctgtg | ctgccgcggc | cgtgccgacg | actgtgccct | gccctacctg | 300 |
| ggcgccatct | gttactgtga | cctcttctgc | aaccgcacgg | tctccgactg | ctgccctgac | 360 |
| tcttgggact | tctgcctcgg | cgtgccaccc | ccttttcccc | cgatccaagg | atgtatgcat | 420 |
| ggaggctcgt | tctatccagt | ccttgggaacg | tactgggaca | actgtaaccg | ttgcacctgc | 480 |
| caggagaaca | ggcagtggca | tggtggatcc | agacatgatc | aaagccatca | accagggcaa | 540 |
| ctatggctgg | caggctggga | accacagcgc | ccttctggggc | atgaccctgg | atgagggcac | 600 |
| tcgctaccgc | ctgggcaaca | tccgccccatc | ttcctcgggtc | atgaacatgc | atgaaattta | 660 |
| tacagtgtct | aaccagggg | aggtgcttcc | cacagccttc | gaggcctctg | agaagtggcc | 720 |
| caacctgatt | catgagcctc | ttgaccaagg | caactgtgca | ggctcctggg | ccttctccac | 780 |
| agcagctgtg | gcatccgatc | gtgtctcaat | ccattctctg | ggacacatga | cgctgtcctt | 840 |
| gtcgcgccag | aacctgtgtg | cctgtgacac | ccaccagcag | cagggtggtc | gcggtgggag | 900 |
| tctcgatggg | gcctgggtgg | tcctgcgtcg | ccaggggtg | gtgtctgacc | actgctaccc | 960 |
| ccttctcggg | cgtgaacgag | acgaggctgg | ccctgcgccc | ccctgtatga | tgcacagccg | 1020 |
| agccatgggt | cggggcaagc | gccaggccac | tgcccactgc | cccaacagct | atgttaataa | 1080 |
| caatgacatc | taccagggtc | ctcctgtcta | ccgcctcggc | tccaacgaca | aggagatcat | 1140 |
| gaaggagctg | atggagaatg | gccctgtcca | agccctcatg | gaggtgcatg | aggacttctt | 1200 |
| cctatacaag | ggaggcatct | acagccacac | gccagtgaag | cctgggaggc | cagagagata | 1260 |
| ccgcctggcat | gggacccact | cagtcaagat | cacaggatgg | ggagaggaga | cgctgccaga | 1320 |
| tggaaggagc | ctcaataact | ggactgcggc | caactcctgg | ggcccagcct | ggggcgagag | 1380 |
| gggccacttc | cgcacgtgac | gcggcggtcaa | tgagtgcgac | atcgagagct | tcgtgctggg | 1440 |
| cgtctggggc | cgcgtgggca | tggaggacat | gggtcatcac | tgaggctgag | ggcaccacgc | 1500 |
| gggggtccgg | ctgggatcca | ggctaagggc | cggcggaaga | ggccccaatg | gggcggtgac | 1560 |
| cccagcctcg | cccgcacagc | cccggggcgc | aggcgggcgc | cagggcgcta | atcccggcgc | 1620 |
| gggttccgct | gacgcagcgc | cccgcctggg | agccgcgggc | aggcgagact | ggcgagagccc | 1680 |
| ccagacctcc | cagtggggac | ggggcagggc | ctggcctggg | aagagcacag | ctgcagatcc | 1740 |
| caggcctctg | gcgccccac | tcaagactac | caaagccagg | acacctcaag | tctccagccc | 1800 |
| caatacccca | ccccaatccc | gtattctttt | tttttttttt | ttagacaggg | tcttgctccg | 1860 |
| ttgcccagg | tggagtgcag | tggcccatca | gggtcactg | taacctccga | ctcctgggtt | 1920 |
| caagtgaacc | tcccacctca | gcctctcaag | tagctgggac | tacaggtgca | ccaccacacc | 1980 |
| tggtctaatt | ttgtattttt | tgtaaagagg | gggtgtctac | tgtgttgccc | aggctgggtt | 2040 |
| cgaactcctg | ggctcaagcg | gtccacctgc | ctccgcctcc | caaagtgtct | ggattgcagg | 2100 |
| catgagccac | tgcacccagc | cctgtattct | tattcttcag | atattttatt | ttcttttcac | 2160 |
| tgtttttaaaa | taaaacaaa | gtattgataa | aaaaaaa | | | 2197 |

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<210> 12
 <211> 164
 <212> PRT
 <213> Homo sapiens

<400> 12
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 Pro Gly Leu His Leu Arg Gly Ile Arg Asp Ala Gly Gly Arg Tyr Cys
 35 40 45
 Gln Glu Gln Asp Leu Cys Cys Arg Gly Arg Ala Asp Asp Cys Ala Leu
 50 55 60
 Pro Tyr Leu Gly Ala Ile Cys Tyr Cys Asp Leu Phe Cys Asn Arg Thr
 65 70 75 80
 Val Ser Asp Cys Cys Pro Asp Phe Trp Asp Phe Cys Leu Gly Val Pro
 85 90 95
 Pro Pro Phe Pro Pro Ile Gln Gly Cys Met His Gly Gly Arg Ile Tyr
 100 105 110
 Pro Val Leu Gly Thr Tyr Trp Asp Asn Cys Asn Arg Cys Thr Cys Gln
 115 120 125
 Glu Asn Arg Gln Trp His Gly Gly Ser Arg His Asp Gln Ser His Gln
 130 135 140
 Pro Gly Gln Leu Trp Leu Ala Gly Trp Glu Pro Gln Arg Leu Leu Gly
 145 150 155 160
 His Asp Pro Gly

<210> 13
 <211> 533
 <212> DNA
 <213> Homo sapiens

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 <221> modified_base
 <222> (33)..(33)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (37)..(37)
 <223> a, t, c or g

<220>
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 <223> a, t, c or g

<220>
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 <222> (94)..(94)
 <223> a, t, c or g

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 <223> a, t, c or g

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 ccaccagcag cagggtctgcc gcgntgggag tctcgatggt gcctgggtgg tcctgcgtcg 180
 ccgaggngtg gtgtctgacc actgctaccc cttctcgggc cgtgaacgag acgaggctgg 240
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 tgcccactgc cccaacagct atgttaataa caatgacatc taccaggtca ctctgttcta 360
 ccgcctcggc tccaacgaca aggagatcat gaaggagctg atggagaatg gccctgtcca 420
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<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 14
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<210> 15
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 15
 ggcggtatct ctctggcctc cc 22

<210> 16
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 16
 ttctccacag cagctgtggc atccgatcgt gtctcaatcc attctctggg 50

<210> 17
 <211> 960
 <212> DNA
 <213> Homo sapiens

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 17

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gctgcttgcc ctgttgatgg caggcttggc cctgcagcca ggcaactgcc tgctgtgcta 60
ctcctgcaaa gcccagggtga gcaacgagga ctgcctgcag gtggagaact gcacccagct 120
gggggagcag tgctggaccg cgcgcattcg cgcagttggc ctctgaccg tcatcagcaa 180
aggctgcagc ttgaactgcg tggatgactc acaggactac tacgtgggca agaagaacat 240
cacgtgctgt gacaccgact tgtgcaacgc cagcggggcc catgccctgc agccggctgc 300
cgccatcctt gcgctgctcc ctgcactcgg cctgctgctc tggggaccg gccagctata 360
ggctctgggg ggccccgctg cagcccacac tgggtgtggt gccccaggcc tctgtgccac 420
tcctcacaga cctggccccag tgggagcctg tcctggttcc tgaggcacat cctaacgcaa 480
gtctgaccat gtagtctgac acccctgtcc cccaccctga ccctcccatg gccctctcca 540
ggactccac ccggcagatc agctctagt acacagatcc gcctgcagat ggccccctcca 600
accctctctg ctgctgtttc catggcccag cattctccac ccttaaccct gtgctcaggc 660
acctcttccc ccaggaagcc ttccctgccc accccatcta tgacttgagc cagggtctggt 720
ccgtggtgtc ccccgacccc agcaggggac aggcaactag gaggggcccag taaaggctga 780
gatgaagtgg actgagtaga actggaggac aagagtcgac gtgagttcct gggagtctcc 840
agagatgggg cctggaggcc tggaggaagg ggccaggcct cacattcgtg gggctccctg 900
aatggcagcc tgagcacagc gtagggcctt aataaacacc tgttgataa gcaaaaaaaa 960

```

<210> 18

<211> 189

<212> PRT

<213> Homo sapiens

<400> 18

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Met Thr His Arg Thr Thr Trp Ala Arg Arg Thr Ser Arg Ala Val
 1          5          10          15

Thr Pro Thr Cys Ala Thr Pro Ala Gly Pro Met Pro Cys Ser Arg Leu
          20          25          30

Pro Pro Ser Leu Arg Cys Ser Leu His Ser Ala Cys Cys Ser Gly Asp
          35          40          45

Pro Ala Ser Tyr Arg Leu Trp Gly Ala Pro Leu Gln Pro Thr Leu Gly
          50          55          60

Val Val Pro Gln Ala Ser Val Pro Leu Leu Thr Asp Leu Ala Gln Trp
          65          70          75          80

Glu Pro Val Leu Val Pro Glu Ala His Pro Asn Ala Ser Leu Thr Met
          85          90          95

Tyr Val Cys Thr Pro Val Pro His Pro Asp Pro Pro Met Ala Leu Ser
          100          105          110

Arg Thr Pro Thr Arg Gln Ile Ser Ser Ser Asp Thr Asp Pro Pro Ala
          115          120          125

Asp Gly Pro Ser Asn Pro Leu Cys Cys Cys Phe His Gly Pro Ala Phe
          130          135          140

Ser Thr Leu Asn Pro Val Leu Arg His Leu Phe Pro Gln Glu Ala Phe
          145          150          155          160

Pro Ala His Pro Ile Tyr Asp Leu Ser Gln Val Trp Ser Val Val Ser
          165          170          175

Pro Ala Pro Ser Arg Gly Gln Ala Leu Arg Arg Ala Gln
          180          185

```

<210> 19

<211> 24

<212> DNA

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 19

tgctgtgcta ctcctgcaaa gccc

24

<210> 20

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 20

tgcacaagtc ggtgtcacag cacg

24

<210> 21

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 21

agcaacgagg actgcctgca ggtggagaac tgcacccagc tggg

44

<210> 22

<211> 1200

<212> DNA

<213> Homo sapiens

<400> 22

| | | | | | | |
|-------------|-------------|------------|------------|------------|------------|------|
| cccacgcgtc | cgaacctctc | cagcgatggg | agccgcccgc | ctgctgcccc | acctcactct | 60 |
| gtgcttacag | ctgctgattc | tctgctgtca | aactcagtag | gtgagggacc | agggcgccat | 120 |
| gaccgaccag | ctgagcaggc | ggcagatccg | cgagtaccaa | ctctacagca | ggaccagtgg | 180 |
| caagcacgtg | caggtcaccg | ggcgtcgcac | ctccgccacc | gccgaggacg | gcaacaagtt | 240 |
| tgccaagctc | atagtggaga | cggacacgtt | tggcagccgg | gttcgcatca | aaggggctga | 300 |
| gagtggagaag | tacatctgta | tgaacaagag | gggcaagctc | atcggaagc | ccagcgggaa | 360 |
| gagcaaagac | tgcgtgttca | cggagatcgt | gctggagaac | aactatacgg | ccttccagaa | 420 |
| cgcccgccac | gagggctggg | tcattggcct | cacgcggcag | gggcggcccc | gccaggcttc | 480 |
| ccgcagccgc | cagaaccagc | gcgaggccca | cttcatcaag | cgctctacc | aaggccagct | 540 |
| gcccttcccc | aaccacgccg | agaagcagaa | gcagttcgag | tttgtgggct | ccgccccac | 600 |
| ccgcccggacc | aagcgcacac | ggcggcccca | gcccctcacg | tagtctggga | ggcagggggc | 660 |
| agcagcccct | gggcccgcctc | cccacccctt | tcccttctta | atccaaggac | tgggctgggg | 720 |
| tggcgggagg | ggagccagat | ccccgaggga | ggaccctgag | ggccgcgaag | catccgagcc | 780 |
| cccagctggg | aaggggcagg | ccggtgcccc | aggggcggct | ggcacagtgc | ccccttccc | 840 |
| gacgggtggc | aggccctgga | gaggaactga | gtgtcacctt | gatctcaggc | caccagcctc | 900 |
| tgccggcctc | ccagccgggc | tcctgaagcc | cgctgaaagg | tcagcgactg | aaggccttgc | 960 |
| agacaaccgt | ctggagggtg | ctgtcctcaa | aatctgtctc | tcggatctcc | ctcagtctgc | 1020 |
| ccccagcccc | caaactcctc | ctggctagac | tgtaggaagg | gacttttgtt | tgtttgtttg | 1080 |
| tttcaggaaa | aaagaaaggg | agagagagga | aaatagaggg | ttgtccactc | ctcacattcc | 1140 |
| acgacccagg | cctgcacccc | acccccaact | cccagccccg | gaataaaacc | attttcctgc | 1200 |

<210> 23

<211> 205

<212> PRT

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Homo sapiens

<400> 23

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Met Gly Ala Ala Arg Leu Leu Pro Asn Leu Thr Leu Cys Leu Gln Leu
 1           5           10           15
Leu Ile Leu Cys Cys Gln Thr Gln Tyr Val Arg Asp Gln Gly Ala Met
          20           25           30
Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser
          35           40           45
Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
          50           55           60
Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp
          65           70           75           80
Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr
          85           90           95
Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
          100          105          110
Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr
          115          120          125
Ala Phe Gln Asn Ala Arg His Glu Gly Trp Phe Met Ala Phe Thr Arg
          130          135          140
Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu
          145          150          155          160
Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn
          165          170          175
His Ala Glu Lys Gln Lys Gln Phe Glu Phe Val Gly Ser Ala Pro Thr
          180          185          190
Arg Arg Thr Lys Arg Thr Arg Arg Pro Gln Pro Leu Thr
          195          200          205

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<210> 24

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 24

cagtacgtga gggaccaggg cgccatga

28

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 25

ccggtgacct gcacgtgctt gcca

24

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<220>

<221> modified_base

<222> (21)..(21)

<223> a, t, c or g

<400> 26

gcggatctgc cgctgtctca nctggctcgg catggcgccc t

41

<210> 27

<211> 2479

<212> DNA

<213> Homo sapiens

<400> 27

| | | | | | | |
|-------------|-------------|-------------|------------|------------|-------------|------|
| acttgccatc | acctgttgcc | agtgtggaaa | aattctccct | gttgaatttt | ttgcacatgg | 60 |
| aggacagcag | caaagagggc | aacacaggct | gataagacca | gagacagcag | ggagattatt | 120 |
| ttaccatacg | ccctcaggac | gttccctcta | gctggagttc | tggacttcaa | cagaacccca | 180 |
| tccagtcatt | ttgattttgc | tgtttatttt | ttttttcttt | ttctttttcc | caccacattg | 240 |
| tattttattt | ccgtacttca | gaaatggggc | tacagaccac | aaagtggccc | agccatgggg | 300 |
| cttttttctt | gaagtcttgg | cttatcattt | ccctggggct | ctactcacag | gtgtccaaac | 360 |
| tcctggcctg | ccctagtgtg | tgccgctgcg | acaggaactt | tgtctactgt | aatgagcgaa | 420 |
| gcttgacctc | agtgcctctt | gggatcccgg | agggcgtaac | cgtactctac | ctccacaaca | 480 |
| accaaaattaa | taatgctgga | tttcctgcag | aactgcacaa | tgtacagtcg | gtgcacacgg | 540 |
| tctacctgta | tggcaaccaa | ctggacgaat | tccccatgaa | ccttcccaag | aatgtcagag | 600 |
| ttctccattt | gcaggaaaac | aatattcaga | ccatttcacg | ggctgctctt | gcccagctct | 660 |
| tgaagcttga | agagctgcac | ctggatgaca | actccatata | cacagtgggg | gtggaagacg | 720 |
| gggccttccg | ggaggctatt | agcctcaaat | tggtgttttt | gtctaagaat | cacctgagca | 780 |
| gtgtgcctgt | tgggcttcct | gtggacttgc | aagagctgag | agtggatgaa | aatcgaattg | 840 |
| ctgtcatatc | cgacatggcc | ttccagaatc | tcacgagctt | ggagcgtctt | attgtggacg | 900 |
| ggaacctcct | gaccaacaag | ggtatcgccg | agggcacctt | cagccatctc | accaagctca | 960 |
| aggaattttc | aattgtacgt | aattcgctgt | cccaccctcc | tcccgatctc | ccaggtagcg | 1020 |
| atctgatcag | gctctatttg | caggacaacc | agataaacca | cattcctttg | acagccttct | 1080 |
| caaactctcg | taagctggaa | cggctggata | tatccaacaa | ccaactgcgg | atgctgactc | 1140 |
| aaggggtttt | tgataatctc | tccaacctga | agcagctcac | tgctcggaat | aacccttggt | 1200 |
| tttgtgactg | cagtattaaa | tgggtcacag | aatggctcaa | atatatccct | tcatctctca | 1260 |
| acgtgcgggg | tttcatgtgc | caaggctctg | aacaagtcgg | ggggatggcc | gtcaggggaat | 1320 |
| taaatatgaa | tcttttgtcc | tgtcccacca | cgacccccgg | cctgcctctc | ttcaccacag | 1380 |
| ccccaaagta | agcttctccg | accactcagc | ctcccaccct | ctctattcca | aacccttagca | 1440 |
| gaagctacac | gcctccaact | cctaccacat | cgaaacttcc | cacgattcct | gactgggatg | 1500 |
| gcagagaaaag | agtgacccca | cctattttctg | aacggatcca | gctctctatc | cattttgtga | 1560 |
| atgatacttc | cattcaagtc | agctggctct | ctctcttcac | cgtgatggca | tacaaactca | 1620 |
| catgggtgaa | aatggggccac | agtttagtag | ggggcatcgt | tcaggagcgc | atagtcagcg | 1680 |
| gtgagaagca | acacctgagc | ctggttaact | tagagccccg | atccacctat | cggatttggt | 1740 |
| tagtgccact | ggatgctttt | aactaccgcg | cggtagaaga | caccatttgt | tcagaggcca | 1800 |
| ccacccatgc | ctcctatctg | aacaacggca | gcaacacagc | gtccagccat | gagcagacga | 1860 |
| cgtcccacag | catgggctcc | ccctttctgc | tggcgggctt | gatcgggggc | gcggtgatat | 1920 |
| ttgtgctggg | ggctcttgctc | agcgtctttt | gctggcatat | gcacaaaaag | gggcgctaca | 1980 |
| cctcccagaa | gtggaaatac | aaccggggcc | ggcggaaaga | tgattattgc | gaggcaggca | 2040 |
| ccaagaagga | caactccatc | ctggagatga | cagaaaccag | ttttcagatc | gtctccttaa | 2100 |
| ataacgatca | actccttaaa | ggagatttca | gactgcagcc | catttacacc | ccaaatgggg | 2160 |
| gcattaatta | cacagactgc | catatcccca | acaacatgcg | atactgcaac | agcagcgtgc | 2220 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|------|
| cagacctgga | gcactgccat | acgtgacagc | cagaggccca | gcggttatcaa | ggcggacaat | 2280 |
| tagactcttg | agaacacact | cgtgtgtgca | cataaagaca | cgcagattac | atttgataaa | 2340 |
| tgttacacag | atgcatttgt | gcatttgaat | actctgtaat | ttatacggtg | tactatataa | 2400 |
| tgggatttaa | aaaaagtgt | atcttttcta | tttcaagtta | attacaaaca | gttttgaac | 2460 |
| tctttgcttt | ttaaattctt | | | | | 2479 |

<210> 28
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Gly Leu Gln Thr Thr Lys Trp Pro Ser His Gly Ala Phe Phe Leu
 1 5 10 15
 Lys Ser Trp Leu Ile Ile Ser Leu Gly Leu Tyr Ser Gln Val Ser Lys
 20 25 30
 Leu Leu Ala Cys Pro Ser Val Cys Arg Cys Asp Arg Asn Phe Val Tyr
 35 40 45
 Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly
 50 55 60
 Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe
 65 70 75 80
 Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr
 85 90 95
 Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg
 100 105 110
 Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala
 115 120 125
 Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser
 130 135 140
 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser
 145 150 155 160
 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val
 165 170 175
 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile
 180 185 190
 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg
 195 200 205
 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly
 210 215 220
 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn
 225 230 235 240
 Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg
 245 250 255
 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe
 260 265 270

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu
275 280 285

Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln
290 300

Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp
305 310 315 320

Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly
325 330 335

Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu
340 345 350

Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Thr Pro Gly Leu Pro
355 360 365

Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro
370 375 380

Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro
385 390 395 400

Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg
405 410 415

Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val
420 425 430

Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met
435 440 445

Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly
450 455 460

Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu
465 470 475 480

Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu
485 490 495

Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala
500 505 510

Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser
515 520 525

His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala
530 535 540

Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser
545 550 555 560

Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys
565 570 575

Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly
580 585 590

Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln
595 600 605

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu
610 615 620
Gln Pro Ile Tyr Thr Pro Asn Gly Gly Ile Asn Tyr Thr Asp Cys His
625 630 635 640
Ile Pro Asn Asn Met Arg Tyr Cys Asn Ser Ser Val Pro Asp Leu Glu
645 650 655
His Cys His Thr
660

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 29
cggctctacct gtatggcaac c 21

<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 30
gcaggacaac cagataaacc ac 22

<210> 31
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 31
acgcagattt gagaaggctg tc 22

<210> 32
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 32
ttcacgggct gctcttgccc agctcttgaa gcttgaagag ctgcac 46

<210> 33
<211> 3449
<212> DNA

<213> Homo

sapiens

<400> 33

| | | | | | | |
|-------------|-------------|-------------|-------------|------------|-------------|------|
| acttgagca | agcggcggcg | gcggagacag | aggcagaggc | agaagctggg | gctccgtcct | 60 |
| cgcctccac | gagcgatccc | cgaggagagc | cgcggccctc | ggcgaggcga | agaggccgac | 120 |
| gaggaagacc | cgggtggctg | cgcccctgcc | tcgcttccca | ggcgccggcg | gctgcagcct | 180 |
| tgcccctctt | gctcgccttg | aaaatggaaa | agatgctcgc | aggctgcttt | ctgctgatcc | 240 |
| tcggacagat | cgtcctcctc | cctgccgagg | ccaggggagcg | gtcacgtggg | aggtccatct | 300 |
| ctaggggag | acacgctcgg | acccaccgcg | agacggccct | tctggagagt | tcctgtgaga | 360 |
| acaagcgggc | agacctgggt | ttcatcattg | acagctctcg | cagtgtcaac | acccatgact | 420 |
| atgcaaaggt | caaggagtgc | atcgtggaca | tcttgcaatt | cttggacatt | ggctctgatg | 480 |
| tcacccgagt | gggcctgctc | caatatggca | gcactgtcaa | gaatgagttc | tcctcaaga | 540 |
| ccttcaagag | gaagtccgag | gtggagcgtg | ctgtcaagag | gatgcggcat | ctgtccacgg | 600 |
| gcaccatgac | tgggctggcc | atccagtatg | ccctgaacat | cgcattctca | gaagcagagg | 660 |
| gggcccggcc | cctgagggag | aatgtgccac | gggtcataat | gatcgtgaca | gatgggagac | 720 |
| ctcaggcagc | cgtggccgag | gtggctgcta | aggcacggga | cacgggcac | ctaattcttg | 780 |
| ccattggtgt | gggcccagga | gacttcaaca | ccttgaagtc | cattgggagt | gagccccatg | 840 |
| aggaccatgt | cttccttggt | gccaatttca | gccagattga | gacgctgacc | tcctgtgttc | 900 |
| agaagaagtt | gtgcacggcc | cacatgtgca | gcaccctgga | gcataactgt | gcccacttct | 960 |
| gcatcaacat | ccctggctca | tacgtctgca | ggtgcaaaca | aggctacatt | ctcaactcgg | 1020 |
| atcagacgac | ttgcagaatc | caggatctgt | gtgccatgga | ggaccacaac | tgtgagcagc | 1080 |
| tctgtgtgaa | tgtgcccggc | tccttcgtct | gccagtgtca | cagtggctac | gccctggctg | 1140 |
| aggatgggaa | gaggtgtgtg | gctgtggact | actgtgcctc | agaaaaccac | ggatgtgaac | 1200 |
| atgagtgtgt | aaatgctgat | ggctcctacc | tttgccagtg | ccatgaagga | tttgtcttta | 1260 |
| acccagatga | aaaaacgtgc | acaaggatca | actactgtgc | actgaacaaa | ccgggctgtg | 1320 |
| agcatgagtg | cgtcaacatg | gaggagagct | actactgccg | ctgccaccgt | ggctacactc | 1380 |
| tggaccccaa | tggcaaaacc | tgcagccgag | tggaccactg | tgcacagcag | gaccatggct | 1440 |
| gtgagcagct | gtgtctgaac | acggaggatt | ccttcgtctg | ccagtgtcca | gaaggcttcc | 1500 |
| tcacaaacga | ggacctcaag | acctgtctcc | gggtggatta | ctgcctgtcg | agtgaccatg | 1560 |
| gttgtgaata | ctcctgtgtc | aacatggaca | gatcctttgc | ctgtcagtgt | cctgaggggac | 1620 |
| acgtgtctcg | cagcgatggg | aagacgtgtg | caaaattgga | ctcttgtgct | ctggggggacc | 1680 |
| acggttgtga | acattcgtgt | gtaagcagtg | aagattcgtt | tgtgtgccag | tgctttgaag | 1740 |
| gttatatact | ccgtgaagat | ggaaaaacct | gcagaaggaa | agatgtctcg | caagctatag | 1800 |
| actatggctg | tgaacacatt | tgtgtgaaca | gtgacgactc | atacagctgc | gagtgcttgg | 1860 |
| agggattccg | gctcgtctgag | gatgggaaac | gctgccgaag | gaaggatgtc | tgcaaatcaa | 1920 |
| cccaccatgg | ctgcgaacac | atttgtgtta | ataatgggaa | ttcctacatc | tgcaaatgct | 1980 |
| cagagggatt | tgttctagct | gaggacggaa | gacggtgcaa | gaaatgcact | gaaggcccaa | 2040 |
| ttgacctggg | ctttgtgatc | gatggatcca | agagtcttgg | agaagagaat | tttgaggctg | 2100 |
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| tggggctgct | ccagtattcc | acacaggtcc | acacagagtt | cactctgaga | aacttcaact | 2220 |
| cagccaaaga | catgaaaaaa | gccgtggccc | acatgaaata | catgggaaag | ggctctatga | 2280 |
| ctgggctggc | cctgaaacac | atgttttgaga | gaagttttac | ccaaggagaa | ggggccaggc | 2340 |
| ccctttccac | aagggtgccc | agagcagcca | ttgtgttcac | cgacggacgg | gctcaggatg | 2400 |
| acgtctccga | gtgggccagt | aaagccaagg | ccaatggtat | cactatgtat | gctgttgggg | 2460 |
| taggaaaagc | cattgaggag | gaactacaag | agattgcctc | tgagcccaca | aacaagcatc | 2520 |
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| tctgtgaagc | tctagaagac | tccgatggaa | gacaggactc | tccagcaggg | gaactgccaa | 2640 |
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| cctgttctaa | ttttgcagtg | caacacagat | atctgtttga | agaagacaat | cttttacggg | 2760 |
| ctacacaaaa | gctttcccat | tcaacaaaac | cttcaggaag | ccctttggaa | gaaaaacacg | 2820 |
| atcaatgcaa | atgtgaaaac | cttataatgt | tccagaacct | tgcaaacgaa | gaagtaagaa | 2880 |
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| gaacgcagtg | cagagcccca | aagctcaggc | tattgttaaa | tcaataatgt | tgtgaagtaa | 3060 |
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| ctgtagaaca | ctggccatag | gaaatgctgt | ttttttgtac | tggactttac | cttgatatat | 3360 |
| gtatatggat | gtatgcataa | aatcatagga | catatgtact | tgtggaacaa | gttggatttt | 3420 |
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<210> 34

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 915

<212> PRT

<213> Homo sapiens

<400> 34

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20 25 30Ser Arg Gly Arg His Ala Arg Thr His Pro Gln Thr Ala Leu Leu Glu
35 40 45Ser Ser Cys Glu Asn Lys Arg Ala Asp Leu Val Phe Ile Ile Asp Ser
50 55 60Ser Arg Ser Val Asn Thr His Asp Tyr Ala Lys Val Lys Glu Phe Ile
65 70 75 80Val Asp Ile Leu Gln Phe Leu Asp Ile Gly Pro Asp Val Thr Arg Val
85 90 95Gly Leu Leu Gln Tyr Gly Ser Thr Val Lys Asn Glu Phe Ser Leu Lys
100 105 110Thr Phe Lys Arg Lys Ser Glu Val Glu Arg Ala Val Lys Arg Met Arg
115 120 125His Leu Ser Thr Gly Thr Met Thr Gly Leu Ala Ile Gln Tyr Ala Leu
130 135 140Asn Ile Ala Phe Ser Glu Ala Glu Gly Ala Arg Pro Leu Arg Glu Asn
145 150 155 160Val Pro Arg Val Ile Met Ile Val Thr Asp Gly Arg Pro Gln Asp Ser
165 170 175Val Ala Glu Val Ala Ala Lys Ala Arg Asp Thr Gly Ile Leu Ile Phe
180 185 190Ala Ile Gly Val Gly Gln Val Asp Phe Asn Thr Leu Lys Ser Ile Gly
195 200 205Ser Glu Pro His Glu Asp His Val Phe Leu Val Ala Asn Phe Ser Gln
210 215 220Ile Glu Thr Leu Thr Ser Val Phe Gln Lys Lys Leu Cys Thr Ala His
225 230 235 240Met Cys Ser Thr Leu Glu His Asn Cys Ala His Phe Cys Ile Asn Ile
245 250 255Pro Gly Ser Tyr Val Cys Arg Cys Lys Gln Gly Tyr Ile Leu Asn Ser
260 265 270Asp Gln Thr Thr Cys Arg Ile Gln Asp Leu Cys Ala Met Glu Asp His
275 280 285Asn Cys Glu Gln Leu Cys Val Asn Val Pro Gly Ser Phe Val Cys Gln
290 295 300Cys Tyr Ser Gly Tyr Ala Leu Ala Glu Asp Gly Lys Arg Cys Val Ala
Page 18

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

305 310 315 320
 Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val
 325 330 335
 Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu
 340 345 350
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 355 360 365
 Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr
 370 375 380
 Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys
 385 390 395 400
 Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu
 405 410 415
 Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe
 420 425 430
 Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu
 435 440 445
 Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser
 450 455 460
 Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys
 465 470 475 480
 Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu
 485 490 495
 His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu
 500 505 510
 Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val
 515 520 525
 Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp
 530 535 540
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 545 550 555 560
 Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly
 565 570 575
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 Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys
 595 600 605
 Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser
 610 615 620
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 625 630 635 640
 Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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660 665 670
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675 680 685
Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser
690 695 700
Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg
705 710 715 720
Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu
725 730 735
Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly
740 745 750
Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro
755 760 765
Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu
770 775 780
Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser
785 790 795 800
Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln
805 810 815
Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu
820 825 830
Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp
835 840 845
Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser
850 855 860
Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu
865 870 875 880
Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln
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Arg Tyr Arg
915

<210> 35

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 35

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gtgaccctgg ttgtgaatac tcc

23

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 36

acagccatgg tctatagctt gg

22

<210> 37

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 37

gcctgtcagt gtcctgaggg acacgtgctc cgcagcgatg ggaag

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<210> 38

<211> 1813

<212> DNA

<213> Homo sapiens

<400> 38

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tttgtatgaa aaa

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1813

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 39
 <211> 390
 <212> PRT
 <213> Homo sapiens

<400> 39
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 35 40 45
 Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln
 50 55 60
 Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys
 65 70 75 80
 Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro
 85 90 95
 Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg
 100 105 110
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 115 120 125
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 130 135 140
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 145 150 155 160
 Gln Gly Val Pro His Val Gly Ala Asn Val Thr Leu Ser Cys Gln Ser
 165 170 175
 Pro Arg Ser Lys Pro Ala Val Gln Tyr Gln Trp Asp Arg Gln Leu Pro
 180 185 190
 Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp Val Ile Arg Gly Ser
 195 200 205
 Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys
 210 215 220
 Lys Ala His Asn Glu Val Gly Thr Ala Gln Cys Asn Val Thr Leu Glu
 225 230 235 240
 Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly
 245 250 255
 Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His
 260 265 270
 Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp
 275 280 285
 Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile
 290 295 300

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Arg
305 310 315 320

Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser
325 330 335

Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly
340 345 350

Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly Gly Val Ser Ser Ser
355 360 365

Gly Leu Ser Arg Met Gly Ala Val Pro Val Met Val Pro Ala Gln Ser
370 375 380

Gln Ala Gly Ser Leu Val
385 390

<210> 40
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 40
agggtctcca ggagaaagac tc 22

<210> 41
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 41
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<210> 42
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 42
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<210> 43
<211> 18
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 43
gtgtgacaca gcgtgggc 18

<210> 44
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 44
gaccggcagg cttctgcg 18

<210> 45
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 45
cagcagcttc agccaccagg agtgg 25

<210> 46
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 46
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<210> 47
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 47
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<210> 48
<211> 2822
<212> DNA
<213> Homo sapiens

<400> 48
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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aa

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<210> 49

<211> 690

<212> PRT

<213> Homo sapiens

<400> 49

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Ser Tyr Thr Gln Asn Cys Thr Lys Thr Pro Cys Leu Pro Asn Ala Lys
          20           25           30

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Cys Glu Ile Arg Asn Gly Ile Glu Ala Cys Tyr Cys Asn Met Gly Phe
          35           40           45

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Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
          50           55           60

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Leu Thr Gln Ser Cys Gly Glu Asn Ala Asn Cys Thr Asn Thr Glu Gly

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 115 120 125
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 325 330 335
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 370 375 380
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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Leu Gly Ile Ile Ile Ser Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr
435 440 445
Phe Trp Phe Phe Ser Glu Ile Gln Ser Thr Arg Thr Thr Ile His Lys
450 455 460
Asn Leu Cys Cys Ser Leu Phe Leu Ala Glu Leu Val Phe Leu Val Gly
465 470 475 480
Ile Asn Thr Asn Thr Asn Lys Leu Phe Cys Ser Ile Ile Ala Gly Leu
485 490 495
Leu His Tyr Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Ile Glu Gly
500 505 510
Ile His Leu Tyr Leu Ile Val Val Gly Val Ile Tyr Asn Lys Gly Phe
515 520 525
Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val
530 535 540
Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys
545 550 555 560
Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly
565 570 575
Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile
580 585 590
Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser
595 600 605
Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu
610 615 620
Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His
625 630 635 640
Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln
645 650 655
Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
660 665 670
Glu Glu Tyr Tyr Arg Leu Phe Lys Asn Val Pro Cys Cys Phe Gly Cys
675 680 685

Leu Arg
690

<210> 50
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<222> (61)..(61)

<223> a, t, c or g

<400> 50

| | | | | | | |
|------------|------------|-------------|-------------|------------|------------|-----|
| tggaacata | tcctccctca | tatgaatatg | gatggagact | acataaatat | atttccaaag | 60 |
| ngaaaagccg | gcatatggat | tcaaattggca | atgttgagc | tgcattttta | tattataaga | 120 |
| gtattggtcc | ctttgctttc | atcatctgac | aacttcttat | tgaaacctca | aaattatgat | 180 |
| aattctgaag | aggaggaaag | agtcatatct | tcagtaattt | cagtctcaat | gagctcaaac | 240 |
| ccaccacat | tatatgaact | tgaaaaata | acatttacat | taagtcacg | aaaggtcaca | 300 |
| gataggtata | ggagtctatg | tggcattttg | gaatactcac | ctgataccat | gaatggcagc | 360 |
| tggctctcag | agggctgtga | gctgacatac | tcaaattgaga | cccacacctc | atgccgctgt | 420 |
| aatcacctga | caatttttgc | aattttgatg | tcctctgggc | cttcatttgg | tattaaagat | 480 |
| tataatattc | ttacaaggat | cactcaacta | ggaataatta | tttactgat | ttgtcttgcc | 540 |
| atatgcattt | ttaccttctg | gttcttcagt | gaaattcaaa | gcaccagga | | 589 |

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 51

ggtaatgagc tccattacag

20

<210> 52

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 52

ggagtagaaa gcgcatgg

18

<210> 53

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 53

cacctgatac catgaatggc ag

22

<210> 54

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 54

cgagctcgaa ttaattcg

18

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 55
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 55
 ggatctcctg agctcagg 18

<210> 56
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 56
 cctagttagag tgatccttgt aag 23

<210> 57
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 57
 atgagaccca cacctcatgc cgctgtaatc acctgacaca ttttgcaatt 50

<210> 58
 <211> 2137
 <212> DNA
 <213> Homo sapiens

<400> 58
 gctcccagcc aagaacctcg gggccgctgc gcggtgggga ggagttcccc gaaacccggc 60
 cgctaagcga ggcctcctcc tcccgcagat ccgaacggcc tgggcggggg caccctggct 120
 gggacaagaa gccgccgcct gcctgccggg gccggggag ggggctgggg ctggggccgg 180
 aggcgggggtg tgagtgggtg tgtgcggggg gcggaggctt gatgcaatcc cgataagaaa 240
 tgctcgggtg tcttgggcac ctacccgtgg ggcccgtgag gcgctactat ataaggctgc 300
 cggcccggag ccgccgcgcc gtcagagcag gagcgtgcg tccaggatct agggccacga 360
 ccatcccaac ccggcactca cagccccgca gcgcattccc gtcgccgccc agcctcccgc 420
 acccccatcg ccggagctgc gccgagagcc ccaggagggt gccatgcgga gcgggtgtgt 480
 ggtggtccac gtatggatcc tggccggcct ctggctggcc gtggccgggc gccccctcgc 540
 cttctcggac gcggggcccc acgtgcacta cggctggggc gaccccatcc gcctgcggca 600
 cctgtacacc tccggccccc acgggctctc cagctgcttc ctgcgcatcc gtgccgacgg 660
 cgctcgtggac tgcgcgcggg gccagagcgc gcacagtttg ctggagatca aggcagtcgc 720
 tctgcggacc gtggccatca agggcgtgca cagcgtgcgg tacctctgca tgggcgccga 780
 cggcaagatg caggggctgc ttcagtactc ggaggaagac tgtgctttcg aggaggagat 840
 ccgcccagat ggctacaatg tgtaccgatc cgagaagcac cgcctcccgg tctccctgag 900
 cagtgccaaa cagcggcagc tgtacaagaa cagaggcttt cttccactct ctcatttcct 960
 gcccatgctg cccatgggtcc cagaggagcc tgaggacctc agggggcact tgggaatctga 1020
 catgttctct tcgcccctgg agaccgacag catggaccca tttgggcttg tcaccggact 1080
 ggaggccgtg aggagtccca gctttgagaa gtaactgaga ccatgcccgg gcctcttcac 1140
 tgctgccagg ggctgtggtg cctgcagcgt gggggacgtg cttctacaag aacagtcctg 1200
 agtccacgtt ctgttttagct ttaggaagaa acatctagaa gttgtacata ttcagagttt 1260

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tccattggca gtgccagttt ctagccaata gacttgtctg atcataacat tgtaagcctg 1320
tagcttgccc agctgctgcc tgggccccca ttctgctccc tcgaggttgc tggacaagct 1380
gctgcactgt ctgagttctg cttgaatacc tccatcgatg gggaactcac ttcctttgga 1440
aaaattctta tgtaagctg aaattctcta attttttctc atcacttccc caggagcagc 1500
cagaagacag gcagtagttt taatttcagg aacaggtgat ccactctgta aaacagcagg 1560
taaatttcac tcaaccccat gtgggaattg atctatatct ctacttccag ggaccatttg 1620
cccttcccaa atccctccag gccagaactg actggagcag gcatggccca ccaggcttca 1680
ggagtagggg aagcctggag cccactcca gccctgggac aacttgagaa ttccccctga 1740
ggccagttct gtcatggatg ctgtcctgag aataacttgc tgtcccggtg tcacctgctt 1800
ccatctccca gccaccagc cctctgccc cctcacatgc ctccccatgg attggggcct 1860
cccaggcccc ccaccttatg tcaacctgca cttcttggtc aaaaatcagg aaaagaaaag 1920
atttgaagac cccaagtctt gtcaataact tgctgtgtgg aagcagcggg ggaagaccta 1980
gaaccctttc cccagcactt ggttttccaa catgatattt atgagtaatt tattttgata 2040
tgtacatctc ttattttctt acattattta tgcccccaa ttatatttat gtatgtaagt 2100
gaggtttgtt ttgtatatta aaatggagtt tgtttgt 2137
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<210> 59
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 59
 Met Arg Ser Gly Cys Val Val Val His Val Trp Ile Leu Ala Gly Leu
 1 5 10 15
 Trp Leu Ala Val Ala Gly Arg Pro Leu Ala Phe Ser Asp Ala Gly Pro
 20 25 30
 His Val His Tyr Gly Trp Gly Asp Pro Ile Arg Leu Arg His Leu Tyr
 35 40 45
 Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
 50 55 60
 Asp Gly Val Val Asp Cys Ala Arg Gly Gln Ser Ala His Ser Leu Leu
 65 70 75 80
 Glu Ile Lys Ala Val Ala Leu Arg Thr Val Ala Ile Lys Gly Val His
 85 90 95
 Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
 100 105 110
 Leu Gln Tyr Ser Glu Glu Asp Cys Ala Phe Glu Glu Glu Ile Arg Pro
 115 120 125
 Asp Gly Tyr Asn Val Tyr Arg Ser Glu Lys His Arg Leu Pro Val Ser
 130 135 140
 Leu Ser Ser Ala Lys Gln Arg Gln Leu Tyr Lys Asn Arg Gly Phe Leu
 145 150 155 160
 Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
 165 170 175
 Glu Asp Leu Arg Gly His Leu Glu Ser Asp Met Phe Ser Ser Pro Leu
 180 185 190
 Glu Thr Asp Ser Met Asp Pro Phe Gly Leu Val Thr Gly Leu Glu Ala
 195 200 205
 Val Arg Ser Pro Ser Phe Glu Lys
 210 215

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 60
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 60
atccgcccag atggctacaa tgtgta 26

<210> 61
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 61
gcctcccggg ctccctgagc agtgccaaac agcggcagtg ta 42

<210> 62
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 62
ccagtccggg gacaagccca aa 22

<210> 63
<211> 1295
<212> DNA
<213> Homo sapiens

<400> 63
cccagaagtt caagggcccc cggcctcctg cgctcctgcc gccgggaccc tcgacctcct 60
cagagcagcc ggctgccgcc ccgggaagat ggcgaggagg agccgccacc gcctcctcct 120
gctgctgctg cgctacctgg tggctgccct gggctatcat aaggcctatg gggtttctgc 180
cccaaaagac caacaagtag tcacagcagt agagtaccaa gaggtatatt tagcctgcaa 240
aaccctaaag aagactgttt cctccagatt agagtgggag aaactgggtc ggagtgtctc 300
ctttgtctac tatcaacaga ctcttcaagg tgattttaaa aatcgagctg agatgataga 360
tttcaatatc cggatcaaaa atgtgacaag aagtgatgcg gggaaatatc gttgtgaagt 420
tagtgcccca tctgagcaag gccaaaacct ggaagaggat acagtcactc tggaagtatt 480
agtggctcca gcagttccat catgtgaagt accctcttct gctctgagtg gaactgtggg 540
agagctacga tgtcaagaca aagaagggaa tccagctcct gaatacacat gggttaagga 600
tggcatccgt ttgctagaaa atcccagact tggctcccaa agcaccaaca gctcatacac 660
aatgaataca aaaactggaa ctctgcaatt taatactgtt tccaaactgg acactggaga 720
atattcctgt gaagcccgcg attctgttgg atatcgagcagg tgcctgggga aacgaatgca 780
agtagatgat ctcaacataa gtggcatcat agcagccgta gtagttgtgg ccttagtgat 840
ttccgtttgt ggccttggtg tatgctatgc tcagaggaaa ggctactttt caaaagaaac 900
ctccttccag aagagtaatt cttcatctaa agccacgaca atgagtgaat atgtgcagtg 960
gctcacgcct gtaatcccag cactttggaa ggccgcggcg ggcggatcac gaggtcagga 1020
gttctagacc agtctggcca atatggtgaa accccatctc tactaaaata caaaaattag 1080
ctgggcatgg tggcatgtgc ctgcagttcc agctgcttgg gagacaggag aatcacttga 1140
acccgggagg cggaggttgc agtgagctga gatcacgcca ctgcagtcca gcctgggtaa 1200

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
cagagcaaga ttccatctca aaaaataaaa taaataaata aataaatact ggtttttacc 1260
tgtagaattc ttacaataaa tatagcttga tattc 1295

<210> 64
<211> 312
<212> PRT
<213> Homo sapiens

<400> 64
Met Ala Arg Arg Ser Arg His Arg Leu Leu Leu Leu Leu Arg Tyr
1 5 10 15
Leu Val Val Ala Leu Gly Tyr His Lys Ala Tyr Gly Phe Ser Ala Pro
20 25 30
Lys Asp Gln Gln Val Val Thr Ala Val Glu Tyr Gln Glu Ala Ile Leu
35 40 45
Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys
50 55 60
Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln
65 70 75 80
Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile
85 90 95
Lys Asn Val Thr Arg Ser Asp Ala Gly Lys Tyr Arg Cys Glu Val Ser
100 105 110
Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu
115 120 125
Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser
130 135 140
Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly
145 150 155 160
Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu
165 170 175
Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met
180 185 190
Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp
195 200 205
Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg
210 215 220
Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile
225 230 235 240
Ile Ala Ala Val Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu
245 250 255
Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser
260 265 270
Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn
275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala
290 295 300

Gly Gly Ser Arg Gly Gln Glu Phe
305 310

<210> 65
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 65
atcgttgtaga agttagtgcc cc 22

<210> 66
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 66
acctgcgata tccaacagaa ttg 23

<210> 67
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 67
ggaagaggat acagtcactc tggaagtatt agtggctcca gcagttcc 48

<210> 68
<211> 2639
<212> DNA
<213> Homo sapiens

<400> 68
gacatcggag gtgggctagc actgaaactg cttttcaaga cgaggaagag gaggagaaag 60
agaaagaaga ggaagatggt gggcaacatt tatTTaacaT gctccacagc ccggaccctg 120
gcatcatgct gctattcctg caaatactga agaagcatgg gatttaaata ttttacttct 180
aaataaatga attactcaat ctccatagac catctataca tactccacct tcaaaaagta 240
catcaatatt atatcattaa ggaaatagta accttctctt ctccaatatg catgacattt 300
ttggacaatg caattgtggc actggcactt atttcagtga agaaaaactt tgtgggttcta 360
tggcattcat catttgacaa atgcaagcat cttccttatc aatcagctcc tattgaactt 420
actagcactg actgtggaat ccttaagggc ccattacatt tctgaagaag aaagctaaga 480
tgaaggacat gccactccga attcatgtgc tacttggcct agctatcact acactagtac 540
aagctgtaga taaaaaagtg gattgtccac ggttatgtac gtgtgaaatc aggccttggt 600
ttacaccagc atccatttat atggaagcat ctacagtgga ttgtaatgat ttaggctctt 660
taactttccc agccagattg ccagctaaca cacagattct tctcctacag actaacaata 720
ttgcaaaaat tgaatactcc acagactttc cagtaaacct tactggcctg gatttatctc 780
aaaacaattt atcttcagtc accaatatta atgtaaaaaa gatgcctcag ctcctttctg 840
tgtacctaga ggaaaacaaa cttactgaac tgcctgaaaa atgtctgtcc gaactgagca 900

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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acttacaaga actctatatatt aatcacaaact tgctttctac aatttcacct ggagccttta 960
ttggcctaca taatctttctt cgacttcattc tcaattcaaa tagattgcag atgatcaaca 1020
gtaagtgggtt tgatgctctt ccaaactctag agattctgat gattggggaa aatccaatta 1080
tcagaatcaa agacatgaac tttaagcctc ttatcaatct tcgcagcctg gttatagctg 1140
gtataaacct cacagaaata ccagataacg ccttggttgg actggaaaac ttagaaagca 1200
tctcttttta cgataacagg cttattaaag taccatgtg tgctcttcaa aaagttgtaa 1260
atctcaaatt tttggatcta aataaaaaatc ctattaatag aatacgaagg ggtgatttta 1320
gcaatatgct acacttaaaa gagttgggga taaataatat gcctgagctg atttccatcg 1380
atagtcttgc tgtggataac ctgccagatt taagaaaaat agaagctact aacaacccta 1440
gattgtctta cattcacccc aatgcatttt tcagactccc caagctggaa tcactcatgc 1500
tgaacagcaa tgctctcagt gccctgtacc atggtaccat tgagtctctg ccaaacctca 1560
aggaaatcag catacacagt aaccccatca ggtgtgactg tgtcatccgt tggatgaaca 1620
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aattccaagg tcagaatggt cggcaagtgc atttcagggg catgatggaa atttgtctcc 1740
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taaattctctg ggaagcagga aaagaaaaaa gtacatcact gaaagtaaaa gcaactgtta 2580
taggtttacc aacaaatatg tcctaaaaac caccaaggaa acctactcca aaaatgaac 2639

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<210> 69
 <211> 708
 <212> PRT
 <213> Homo sapiens

<400> 69
 Met Lys Asp Met Pro Leu Arg Ile His Val Leu Leu Gly Leu Ala Ile
 1 5 10 15
 Thr Thr Leu Val Gln Ala Val Asp Lys Lys Val Asp Cys Pro Arg Leu
 20 25 30
 Cys Thr Cys Glu Ile Arg Pro Trp Phe Thr Pro Arg Ser Ile Tyr Met
 35 40 45
 Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro
 50 55 60
 Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn
 65 70 75 80
 Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
 85 90 95
 Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val
 100 105 110
 Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu
 115 120 125
 Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu
 130 135 140

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe
145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu
165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile
180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe
195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu
210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser
225 230 235 240

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu
245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile
260 265 270

Asn Arg Ile Arg Arg Gly Asp Phe Ser Asn Met Leu His Leu Lys Glu
275 280 285

Leu Gly Ile Asn Asn Met Pro Glu Leu Ile Ser Ile Asp Ser Leu Ala
290 295 300

Val Asp Asn Leu Pro Asp Leu Arg Lys Ile Glu Ala Thr Asn Asn Pro
305 310 315 320

Arg Leu Ser Tyr Ile His Pro Asn Ala Phe Phe Arg Leu Pro Lys Leu
325 330 335

Glu Ser Leu Met Leu Asn Ser Asn Ala Leu Ser Ala Leu Tyr His Gly
340 345 350

Thr Ile Glu Ser Leu Pro Asn Leu Lys Glu Ile Ser Ile His Ser Asn
355 360 365

Pro Ile Arg Cys Asp Cys Val Ile Arg Trp Met Asn Met Asn Lys Thr
370 375 380

Asn Ile Arg Phe Met Glu Pro Asp Ser Leu Phe Cys Val Asp Pro Pro
385 390 395 400

Glu Phe Gln Gly Gln Asn Val Arg Gln Val His Phe Arg Asp Met Met
405 410 415

Glu Ile Cys Leu Pro Leu Ile Ala Pro Glu Ser Phe Pro Ser Asn Leu
420 425 430

Asn Val Glu Ala Gly Ser Tyr Val Ser Phe His Cys Arg Ala Thr Ala
435 440 445

Glu Pro Gln Pro Glu Ile Tyr Trp Ile Thr Pro Ser Gly Gln Lys Leu
450 455 460

Leu Pro Asn Thr Leu Thr Asp Lys Phe Tyr Val His Ser Glu Gly Thr
465 470 475 480

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Asp Ile Asn Gly Val Thr Pro Lys Glu Gly Gly Leu Tyr Thr Cys
485 490 495

Ile Ala Thr Asn Leu Val Gly Ala Asp Leu Lys Ser Val Met Ile Lys
500 505 510

Val Asp Gly Ser Phe Pro Gln Asp Asn Asn Gly Ser Leu Asn Ile Lys
515 520 525

Ile Arg Asp Ile Gln Ala Asn Ser Val Leu Val Ser Trp Lys Ala Ser
530 535 540

Ser Lys Ile Leu Lys Ser Ser Val Lys Trp Thr Ala Phe Val Lys Thr
545 550 555 560

Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys
565 570 575

Val Tyr Asn Leu Thr His Leu Asn Pro Ser Thr Glu Tyr Lys Ile Cys
580 585 590

Ile Asp Ile Pro Thr Ile Tyr Gln Lys Asn Arg Lys Lys Cys Val Asn
595 600 605

Val Thr Thr Lys Gly Leu His Pro Asp Gln Lys Glu Tyr Glu Lys Asn
610 615 620

Asn Thr Thr Thr Leu Met Ala Cys Leu Gly Gly Leu Leu Gly Ile Ile
625 630 635 640

Gly Val Ile Cys Leu Ile Ser Cys Leu Ser Pro Glu Met Asn Cys Asp
645 650 655

Gly Gly His Ser Tyr Val Arg Asn Tyr Leu Gln Lys Pro Thr Phe Ala
660 665 670

Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
675 680 685

Glu Lys Ser Thr Ser Leu Lys Val Lys Ala Thr Val Ile Gly Leu Pro
690 695 700

Thr Asn Met Ser
705

<210> 70

<211> 1305

<212> DNA

<213> Homo sapiens

<400> 70

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| gcccgggact | ggcgcaaggt | gcccgaagcaa | ggaaagaaat | aatgaagaga | cacatgtgtt | 60 |
| agctgcagcc | ttttgaaaca | cgcaagaagg | aaatcaatag | tgtggacagg | gctggaacct | 120 |
| ttaccacgt | tggtggagta | gatgaggaat | gggctcgtga | ttatgctgac | attccagcat | 180 |
| gaatctggta | gacctgtggt | taaccgcgtt | cctctccatg | tgtctcctcc | tacaaagttt | 240 |
| tggtcttatg | atactgtgct | ttcattctgc | cagtatgtgt | cccaagggct | gtctttgttc | 300 |
| ttcctctggg | ggtttaaatg | tcacctgtag | caatgcaaat | ctcaaggaaa | tacctagaga | 360 |
| tcttctcct | gaaacagtct | tactgtatct | ggactccaat | cagatcacat | ctattcccaa | 420 |
| tgaaattttt | aaggacctcc | atcaactgag | agttctcaac | ctgtccaaaa | atggcattga | 480 |
| gtttatcgat | gagcatgcct | tcaaaggagt | agctgaaacc | ttgcagactc | tggacttgct | 540 |
| cgacaatcgg | attcaaagtg | tgcacaaaaa | tgcttcaat | aacctgaagg | ccagggccag | 600 |
| aattgccaac | aacccctggc | actgcgactg | tactctacag | caagttctga | ggagcatggc | 660 |
| gtccaatcat | gagacagccc | acaacgtgat | ctgtaaaacg | tccgtgttgg | atgaacatgc | 720 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tggcagacca ttcctcaatg ctgccaacga cgctgacctt tgtaacctcc ctaaaaaac 780
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cctgccaagc aggcagaaga aagcagatga acctgatgat attagcactg tggatatagt 960
tccaaactga ctgtcattga gaaagaaaga aagtagtttg cgattgcagt agaaataagt 1020
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tatgccactg ctgaactttt aacaaacact acaacataaa taatttgagt ttaggtgatc 1140
caccctttaa ttgtaccccc gatggtatat ttctgagtaa gctactatct gaacattagt 1200
tagatccatc tcactattta ataatgaaat ttatTTTTTT aattttaaag caaataaaag 1260
cttaactttg aaccatggga aaaaaaaaaa aaaaaaaaaa aaaca 1305

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<210> 71
 <211> 259
 <212> PRT
 <213> Homo sapiens

<400> 71
 Met Asn Leu Val Asp Leu Trp Leu Thr Arg Ser Leu Ser Met Cys Leu
 1 5 10 15
 Leu Leu Gln Ser Phe Val Leu Met Ile Leu Cys Phe His Ser Ala Ser
 20 25 30
 Met Cys Pro Lys Gly Cys Leu Cys Ser Ser Ser Gly Gly Leu Asn Val
 35 40 45
 Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro
 50 55 60
 Glu Thr Val Leu Leu Tyr Leu Asp Ser Asn Gln Ile Thr Ser Ile Pro
 65 70 75 80
 Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser
 85 90 95
 Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala
 100 105 110
 Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val
 115 120 125
 His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn
 130 135 140
 Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met
 145 150 155 160
 Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val
 165 170 175
 Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala
 180 185 190
 Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val
 195 200 205
 Thr Met Phe Gly Trp Phe Thr Met Val Ile Ser Tyr Val Val Tyr Tyr
 210 215 220
 Val Arg Gln Asn Gln Glu Asp Ala Arg Arg His Leu Glu Tyr Leu Lys
 225 230 235 240
 Ser Leu Pro Ser Arg Gln Lys Lys Ala Asp Glu Pro Asp Asp Ile Ser

Thr Val Val

<210> 72
<211> 2290
<212> DNA
<213> Homo sapiens

<400> 72
accgagccga gcggaccgaa ggcgcgcccc agatgcaggt gagcaagagg atgctggcgg 60
ggggcgtag gagcatgccc agccccctcc tggcctgctg gcagcccatc ctcctgctgg 120
tgctgggctc agtgcgtgca ggctcgccca cgggctgccc gccccgctgc gaggctccc 180
cccaggaccg cgctgtgctg tgccaccgca agtgccttgg ggcagtcctc gaggggcatcc 240
ccaccgagac gcgcctgctg gacctaggca agaaccgcat caaaacgctc aaccaggacg 300
agttcgccag cttcccgcac ctggaggagc tggagctcaa cgagaacatc gtgagcgccg 360
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gcctgaagct catcccgcta ggcgtcttca ctggcctcag caacctgacc aagcaggaca 480
tcagcgagaa caagatcggt atcctactgg actacatggt tcaggacctg tacaacctca 540
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tcaacagcct ggagcagctg acgctggaga aatgcaacct gacctccatc cccaccgagg 660
cgctgtccca cctgcacggc ctcactgctc tggagctccg gcacctcaac atcaatgcca 720
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gcttctcaa cctctcctac aacccccatca gcaccattga gggctccatg ttgcatgagc 960
tgctccggct gcaggagatc cagctgggtg gcgggcagct ggccgtggtg gagccctatg 1020
ccttccgcgg cctcaactac ctgcgcgtgc tcaatgtctc tggcaaccag ctgaccacac 1080
tggaggaatc agtcttccac tcggtgggca acctggagac actcatctg gactccaacc 1140
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ggaccccacc tacacagggg cattgacaga ctggagtga aagccgacga accgacacgc 2160
ggcagagtca ataattcaat aaaaaagtta cgaactttct ctgtaacttg ggtttcaata 2220
attatggatt tttatgaaaa cttgaaataa taaaaagaga aaaaaactaa aaaaaaaaaa 2280
aaaaaaaaa 2290

<210> 73
<211> 620
<212> PRT
<213> Homo sapiens

<400> 73
Met Gln Val Ser Lys Arg Met Leu Ala Gly Gly Val Arg Ser Met Pro
1 5 10 15
Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile Leu Leu Leu Val Leu Gly
20 25 30

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Val Leu Ser Gly Ser Ala Thr Gly Cys Pro Pro Arg Cys Glu Cys
35 40 45

Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Cys Phe Val Ala
50 55 60

Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
65 70 75 80

Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
85 90 95

Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
100 105 110

Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
115 120 125

Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
130 135 140

Leu Thr Lys Gln Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
145 150 155 160

Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
165 170 175

Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
180 185 190

Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
195 200 205

Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
210 215 220

Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
225 230 235 240

Leu Lys Val Leu Glu Ile Ser His Trp Pro Tyr Leu Asp Thr Met Thr
245 250 255

Pro Asn Cys Leu Tyr Gly Leu Asn Leu Thr Ser Leu Ser Ile Thr His
260 265 270

Cys Asn Leu Thr Ala Val Pro Tyr Leu Ala Val Arg His Leu Val Tyr
275 280 285

Leu Arg Phe Leu Asn Leu Ser Tyr Asn Pro Ile Ser Thr Ile Glu Gly
290 295 300

Ser Met Leu His Glu Leu Leu Arg Leu Gln Glu Ile Gln Leu Val Gly
305 310 315 320

Gly Gln Leu Ala Val Val Glu Pro Tyr Ala Phe Arg Gly Leu Asn Tyr
325 330 335

Leu Arg Val Leu Asn Val Ser Gly Asn Gln Leu Thr Thr Leu Glu Glu
340 345 350

Ser Val Phe His Ser Val Gly Asn Leu Glu Thr Leu Ile Leu Asp Ser
355 360 365

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Asn Pro Leu Ala Cys Asp Cys Arg Leu Leu Trp Val Phe Arg Arg Arg
 370 375 380

Trp Arg Leu Asn Phe Asn Arg Gln Gln Pro Thr Cys Ala Thr Pro Glu
 385 390 395 400

Phe Val Gln Gly Lys Glu Phe Lys Asp Phe Pro Asp Val Leu Leu Pro
 405 410 415

Asn Tyr Phe Thr Cys Arg Arg Ala Arg Ile Arg Asp Arg Lys Ala Gln
 420 425 430

Gln Val Phe Val Asp Glu Gly His Thr Val Gln Phe Val Cys Arg Ala
 435 440 445

Asp Gly Asp Pro Pro Pro Ala Ile Leu Trp Leu Ser Pro Arg Lys His
 450 455 460

Leu Val Ser Ala Lys Ser Asn Gly Arg Leu Thr Val Phe Pro Asp Gly
 465 470 475 480

Thr Leu Glu Val Arg Tyr Ala Gln Val Gln Asp Asn Gly Thr Tyr Leu
 485 490 495

Cys Ile Ala Ala Asn Ala Gly Gly Asn Asp Ser Met Pro Ala His Leu
 500 505 510

His Val Arg Ser Tyr Ser Pro Asp Trp Pro His Gln Pro Asn Lys Thr
 515 520 525

Phe Ala Phe Ile Ser Asn Gln Pro Gly Glu Gly Glu Ala Asn Ser Thr
 530 535 540

Arg Ala Thr Val Pro Phe Pro Phe Asp Ile Lys Thr Leu Ile Ile Ala
 545 550 555 560

Thr Thr Met Gly Phe Ile Ser Phe Leu Gly Val Val Leu Phe Cys Leu
 565 570 575

Val Leu Leu Phe Leu Trp Ser Arg Gly Lys Gly Asn Thr Lys His Asn
 580 585 590

Ile Glu Ile Glu Tyr Val Pro Arg Lys Ser Asp Ala Gly Ile Ser Ser
 595 600 605

Ala Asp Ala Pro Arg Lys Phe Asn Met Lys Met Ile
 610 615 620

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 74

tcacctggag cctttattgg cc

22

<210> 75

<211> 23

<212> DNA

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 75

ataccagcta taaccaggct gcg

23

<210> 76

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 76

caacagtaag tggtttgatg ctcttccaaa tctagagatt ctgatgattg
gg

50
52

<210> 77

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 77

ccatgtgtct cctcctacaa ag

22

<210> 78

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 78

gggaatagat gtgatctgat tgg

23

<210> 79

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 79

cacctgtagc aatgcaaadc tcaaggaaat acctagagat cttcctcctg

50

<210> 80

<211> 22

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 80

agcaaccgcc tgaagctcat cc

22

<210> 81

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 81

aaggcgcggt gaaagatgta gacg

24

<210> 82

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 82

gactacatgt ttcaggacct gtacaacctc aagtcactgg aggttggcga

50

<210> 83

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 83

| | | | | | | |
|------------|-------------|------------|-------------|-------------|-------------|------|
| cccacgcgtc | cgcacctcgg | ccccgggctc | cgaagcggct | cggggggcgc | ctttcgggtca | 60 |
| acatcgtagt | ccacccccctc | cccatcccca | gcccccgggg | attcaggctc | gccagcgccc | 120 |
| agccaggagg | ccggcccgga | agcgcgatgg | gggccccagc | cgctcgcctc | ctgctcctgc | 180 |
| tcctgctggt | cgcctgctgc | tgggcgcccc | gcggggccaa | cctctcccag | gacgacagcc | 240 |
| agccctggac | atctgatgaa | acagtgggtg | ctgggtggcac | cgtgggtgctc | aagtgccaaag | 300 |
| tgaaagatca | cgaggactca | tccctgcaat | ggtctaacc | tgctcagcag | actctctact | 360 |
| ttggggagaa | gagagccctt | cgagataatc | gaattcagct | ggttacctct | acgccccacg | 420 |
| agctcagcat | cagcatcagc | aatgtggccc | tggcagacga | gggcgagtag | acctgctcaa | 480 |
| tcttcactat | gcctgtgcga | actgccaaat | ccctcgtcac | tgtgctagga | attccacaga | 540 |
| agcccatcat | cactgggtat | aaatcttcat | tacgggaaaa | agacacagcc | accctaaact | 600 |
| gtcagtcttc | tgggagcaag | cctgcagccc | ggctcacctg | gagaaagggg | gaccaagaac | 660 |
| tccacggaga | accaacccgc | atacaggaag | atcccaatgg | taaaaccttc | actgtcagca | 720 |
| gctcggtgac | attccaggtt | acccgggagg | atgatggggc | gagcatcggt | tgctctgtga | 780 |
| accatgaatc | tctaaaggga | gctgacagat | ccacctctca | acgcattgaa | gttttataca | 840 |
| caccaactgc | gatgattagg | ccagaccctc | cccactcctc | tgagggccag | aagctgttgc | 900 |
| tacactgtga | gggtcgcggc | aatccagtcc | cccagcagta | cctatgggag | aaggagggca | 960 |
| gtgtgccacc | cctgaagatg | acccaggaga | gtgccctgat | cttccctttc | ctcaacaaga | 1020 |
| gtgacagtgg | cacctacggc | tgcacagcca | ccagcaacat | gggcagctac | aaggcctact | 1080 |
| acaccctcaa | tgtaaatgac | cccagtcagg | tgccctcctc | ctccagcacc | taccacgcca | 1140 |
| tcacgcgtgg | gatcgtggct | ttcattgtct | tcctgctgct | catcatgctc | atcttccttg | 1200 |
| gccactactt | gatccggcac | aaaggaacct | acctgacaca | tgaggcaaaa | ggctccgacg | 1260 |
| atgctccaga | cgcggaacg | gccatcatca | atgcagaagg | cgggcagtca | ggagggggacg | 1320 |
| acaagaagga | atatttcac | tagaggcgcc | tgcccacttc | ctgcgcccc | cagggggccct | 1380 |
| gtggggactg | ctggggccgt | caccaaccgc | gacttgatca | gagcaaccgc | agggccgccc | 1440 |
| ctccccgctg | ctccccagcc | caccaccccc | cctgtacaga | atgtctgctt | tgggtgcggt | 1500 |
| tttgactctg | gtttggaatg | gggagggagg | agggcggggg | gaggggaggg | ttgccctcag | 1560 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
 ccctttccgt ggcttctctg catttgggtt attattattt ttgtaacaat ccctaatcaa 1620
 atctgtctcc aggctggaga ggcaggagcc ctggggtgag aaaagcaaaa aacaaacaaa 1680
 aaaca 1685

<210> 84
 <211> 398
 <212> PRT
 <213> Homo sapiens

<400> 84
 Met Gly Ala Pro Ala Ala Ser Leu Leu Leu Leu Leu Leu Phe Ala
 1 5 10 15
 Cys Cys Trp Ala Pro Gly Gly Ala Asn Leu Ser Gln Asp Asp Ser Gln
 20 25 30
 Pro Trp Thr Ser Asp Glu Thr Val Val Ala Gly Gly Thr Val Val Leu
 35 40 45
 Lys Cys Gln Val Lys Asp His Glu Asp Ser Ser Leu Gln Trp Ser Asn
 50 55 60
 Pro Ala Gln Gln Thr Leu Tyr Phe Gly Glu Lys Arg Ala Leu Arg Asp
 65 70 75 80
 Asn Arg Ile Gln Leu Val Thr Ser Thr Pro His Glu Leu Ser Ile Ser
 85 90 95
 Ile Ser Asn Val Ala Leu Ala Asp Glu Gly Glu Tyr Thr Cys Ser Ile
 100 105 110
 Phe Thr Met Pro Val Arg Thr Ala Lys Ser Leu Val Thr Val Leu Gly
 115 120 125
 Ile Pro Gln Lys Pro Ile Ile Thr Gly Tyr Lys Ser Ser Leu Arg Glu
 130 135 140
 Lys Asp Thr Ala Thr Leu Asn Cys Gln Ser Ser Gly Ser Lys Pro Ala
 145 150 155 160
 Ala Arg Leu Thr Trp Arg Lys Gly Asp Gln Glu Leu His Gly Glu Pro
 165 170 175
 Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser
 180 185 190
 Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val
 195 200 205
 Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser
 210 215 220
 Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp
 225 230 235 240
 Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu Leu His Cys Glu Gly
 245 250 255
 Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser
 260 265 270
 Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe
 275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn
290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser
305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile
325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly
340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys
355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu
370 375 380

Gly Gly Gln Ser Gly Gly Asp Asp Lys Lys Glu Tyr Phe Ile
385 390 395

<210> 85

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 85

gctaggaatt ccacagaagc cc

22

<210> 86

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 86

aacctggaat gtcaccgagc tg

22

<210> 87

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 87

cctagcacag tgacgaggga cttggc

26

<210> 88

<211> 50

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 88

aagacacagc caccctaaac tgtcagtctt ctgggagcaa gcctgcagcc 50

<210> 89

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 89

gccctggcag acgagggcga gtacacctgc tcaatcttca ctatgcctgt 50

<210> 90

<211> 2755

<212> DNA

<213> Homo sapiens

<400> 90

| | | | | | | |
|-------------|------------|-------------|-------------|-------------|-------------|------|
| ggggggttagg | gaggaaggaa | tccaccccca | cccccccaa | cccttttctt | ctcctttcct | 60 |
| ggcttcggac | attggagcac | taaatgaact | tgaattgtgt | ctgtggcgag | caggatgggtc | 120 |
| gctgttactt | tgtgatgaga | tcggggatga | attgctcgct | ttaaaaatgc | tgctttggat | 180 |
| tctgttgctg | gagacgtctc | tttgttttgc | cgctggaaac | gttacagggg | acgtttgcaa | 240 |
| agagaagatc | tgttcctgca | atgagataga | aggggacctt | cacgtagact | gtgaaaaaaaa | 300 |
| gggcttcaca | agtctgcagc | gtttcactgc | cccgaacttc | cagttttacc | atatttttct | 360 |
| gcatggcaat | tccctcactc | gacttttccc | taatgagttc | gctaactttt | ataatgcggt | 420 |
| tagtttgca | atggaaaaca | atggcttgca | tgaatcggtt | ccgggggctt | ttctggggct | 480 |
| gcagctgggtg | aaaagggtgc | acatcaacaa | caacaagatc | aagtcttttc | gaaagcagac | 540 |
| ttttctgggg | ctggacgatc | tggaatatct | ccaggctgat | tttaatttat | tacgagatat | 600 |
| agacccgggg | gccttcagg | acttgaacaa | gctggagggtg | ctcattttta | atgacaatct | 660 |
| catcagcacc | ctacctgcca | acgtgttcca | gtatgtgccc | atcacccacc | tcgacctccg | 720 |
| gggtaacagg | ctgaaaacgc | tgccctatga | ggagggtcttg | gagcaaattcc | ctgggtattgc | 780 |
| ggagatcctg | ctagaggata | acccttgagg | ctgcacctgt | gatctgctct | ccctgaaaga | 840 |
| atggctggaa | aacattccca | agaatgccct | gatcggccga | gtgggtctcg | aagccccac | 900 |
| cagactgcag | ggtaaagacc | tcaatgaaac | caccgaacag | gacttgtgtc | ctttgaaaaa | 960 |
| ccgagtggat | tctagtctcc | cggcgccccc | tgcccaagaa | gagacctttg | ctcctggacc | 1020 |
| cctgcgaact | cctttcaaga | caaatgggca | agaggatcat | gccacaccag | gggtctgctcc | 1080 |
| aaacggagggt | acaaagatcc | caggcaactg | gcagatcaaa | atcagaccca | cagcagcgat | 1140 |
| agcgacgggt | agctccagga | acaaaccctt | agctaacagt | ttaccctgcc | ctggggggctg | 1200 |
| cagctgcgac | cacatcccag | ggctcgggtt | aaagatgaac | tgcaacaaca | ggaacgtgag | 1260 |
| cagcttggct | gatttgaagc | ccaagctctc | taacgtgcag | gagcttttcc | tacgagataa | 1320 |
| caagatccac | agcatccgaa | aatcgcaact | tgtggattac | aagaacctca | ttctgttgga | 1380 |
| tctgggcaac | aataacatcg | ctactgtaga | gaacaacact | ttcaagaacc | ttttggacct | 1440 |
| cagggtggcta | tacatggata | gcaattacct | ggacacgctg | tcccgggaga | aattcgcggtg | 1500 |
| gctgcaaaac | ctagagtacc | tgaacgtgga | gtacaacgct | atccagctca | tcctcccggg | 1560 |
| cactttcaat | gccatgccca | aactgaggat | cctcattctc | aacaacaacc | tgctgagggtc | 1620 |
| cctgcctgtg | gacgtgttcg | ctgggggtctc | gctctctaaa | ctcagcctgc | acaacaatta | 1680 |
| cttcatgtac | ctcccgggtg | caggggtgct | ggaccagtta | acctccatca | tccagataga | 1740 |
| cctccacgga | aacccctggg | agtgtcctcg | cacaattgtg | cctttcaagc | agtgggcaga | 1800 |
| acgcttgggt | tccgaagtgc | tgatgagcga | cctcaagtgt | gagacgccgg | tgaacttctt | 1860 |
| tagaaaggat | ttcatgctcc | tctccaatga | cgagatctgc | cctcagctgt | acgctaggat | 1920 |
| ctcggccacg | ttaacttcgc | acagtaaaaa | cagcactggg | ttggcggaga | ccgggacgca | 1980 |
| ctccaactcc | tacctagaca | ccagcagggt | gtccatctcg | gtgttggtcc | cgggactgtc | 2040 |
| gctggtgttt | gtcacctccg | ccttcaccgt | ggtgggcatg | ctcgtgttta | tcctgaggaa | 2100 |
| ccgaaaagcgg | tccaagagac | gagatgccaa | ctctctcccg | tccgagatta | attccctaca | 2160 |
| gacagtctgt | gactcttcct | actggcaca | tgggccttac | aacgcagatg | gggcccacag | 2220 |
| agtgtatgac | tgtggctctc | actcgtctc | agactaagac | cccaacccca | ataggggagg | 2280 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gcagaggggaa ggcgatacat ccttccccac cgcaggcacc ccgggggctg gaggggcgtg 2340
taccCAAATC CCCGCGCCAT CAGCCTGGAT GGGCATAAGT AGATAAATAA CTGTGAGCTC 2400
gcacaaccga aagggcctga ccccttactt agctccctcc ttgaaacaaa gagcagactg 2460
tgagagagctg ggagagcgca gccagctcgc tctttgctga gagccccctt tgacagaaag 2520
cccagcacga ccctgctgga agaactgaca gtgccctcgc cctcggcccc ggggcctgtg 2580
gggttggatg ccgcggttct atacatatat acatatatcc acatctatat agagagatag 2640
atatctatctt ttcccctgtg gattagcccc gtgatggctc cctgttggct acgcagggat 2700
gggcagttgc acgaaggcat gaatgtattg taaataagta actttgactt ctgac 2755
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<210> 91
 <211> 696
 <212> PRT
 <213> Homo sapiens

<400> 91
 Met Leu Leu Trp Ile Leu Leu Leu Glu Thr Ser Leu Cys Phe Ala Ala
 1 5 10 15
 Gly Asn Val Thr Gly Asp Val Cys Lys Glu Lys Ile Cys Ser Cys Asn
 20 25 30
 Glu Ile Glu Gly Asp Leu His Val Asp Cys Glu Lys Lys Gly Phe Thr
 35 40 45
 Ser Leu Gln Arg Phe Thr Ala Pro Thr Ser Gln Phe Tyr His Leu Phe
 50 55 60
 Leu His Gly Asn Ser Leu Thr Arg Leu Phe Pro Asn Glu Phe Ala Asn
 65 70 75 80
 Phe Tyr Asn Ala Val Ser Leu His Met Glu Asn Asn Gly Leu His Glu
 85 90 95
 Ile Val Pro Gly Ala Phe Leu Gly Leu Gln Leu Val Lys Arg Leu His
 100 105 110
 Ile Asn Asn Asn Lys Ile Lys Ser Phe Arg Lys Gln Thr Phe Leu Gly
 115 120 125
 Leu Asp Asp Leu Glu Tyr Leu Gln Ala Asp Phe Asn Leu Leu Arg Asp
 130 135 140
 Ile Asp Pro Gly Ala Phe Gln Asp Leu Asn Lys Leu Glu Val Leu Ile
 145 150 155 160
 Leu Asn Asp Asn Leu Ile Ser Thr Leu Pro Ala Asn Val Phe Gln Tyr
 165 170 175
 Val Pro Ile Thr His Leu Asp Leu Arg Gly Asn Arg Leu Lys Thr Leu
 180 185 190
 Pro Tyr Glu Glu Val Leu Glu Gln Ile Pro Gly Ile Ala Glu Ile Leu
 195 200 205
 Leu Glu Asp Asn Pro Trp Asp Cys Thr Cys Asp Leu Leu Ser Leu Lys
 210 215 220
 Glu Trp Leu Glu Asn Ile Pro Lys Asn Ala Leu Ile Gly Arg Val Val
 225 230 235 240
 Cys Glu Ala Pro Thr Arg Leu Gln Gly Lys Asp Leu Asn Glu Thr Thr
 245 250 255

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
 Glu Gln Asp Leu Cys Pro Leu Lys Asn Arg Val Asp Ser Ser Leu Pro
 260 265 270

Ala Pro Pro Ala Gln Glu Glu Thr Phe Ala Pro Gly Pro Leu Pro Thr
 275 280 285

Pro Phe Lys Thr Asn Gly Gln Glu Asp His Ala Thr Pro Gly Ser Ala
 290 295 300

Pro Asn Gly Gly Thr Lys Ile Pro Gly Asn Trp Gln Ile Lys Ile Arg
 305 310 315 320

Pro Thr Ala Ala Ile Ala Thr Gly Ser Ser Arg Asn Lys Pro Leu Ala
 325 330 335

Asn Ser Leu Pro Cys Pro Gly Gly Cys Ser Cys Asp His Ile Pro Gly
 340 345 350

Ser Gly Leu Lys Met Asn Cys Asn Asn Arg Asn Val Ser Ser Leu Ala
 355 360 365

Asp Leu Lys Pro Lys Leu Ser Asn Val Gln Glu Leu Phe Leu Arg Asp
 370 375 380

Asn Lys Ile His Ser Ile Arg Lys Ser His Phe Val Asp Tyr Lys Asn
 385 390 395 400

Leu Ile Leu Leu Asp Leu Gly Asn Asn Asn Ile Ala Thr Val Glu Asn
 405 410 415

Asn Thr Phe Lys Asn Leu Leu Asp Leu Arg Trp Leu Tyr Met Asp Ser
 420 425 430

Asn Tyr Leu Asp Thr Leu Ser Arg Glu Lys Phe Ala Gly Leu Gln Asn
 435 440 445

Leu Glu Tyr Leu Asn Val Glu Tyr Asn Ala Ile Gln Leu Ile Leu Pro
 450 455 460

Gly Thr Phe Asn Ala Met Pro Lys Leu Arg Ile Leu Ile Leu Asn Asn
 465 470 475 480

Asn Leu Leu Arg Ser Leu Pro Val Asp Val Phe Ala Gly Val Ser Leu
 485 490 495

Ser Lys Leu Ser Leu His Asn Asn Tyr Phe Met Tyr Leu Pro Val Ala
 500 505 510

Gly Val Leu Asp Gln Leu Thr Ser Ile Ile Gln Ile Asp Leu His Gly
 515 520 525

Asn Pro Trp Glu Cys Ser Cys Thr Ile Val Pro Phe Lys Gln Trp Ala
 530 535 540

Glu Arg Leu Gly Ser Glu Val Leu Met Ser Asp Leu Lys Cys Glu Thr
 545 550 555 560

Pro Val Asn Phe Phe Arg Lys Asp Phe Met Leu Leu Ser Asn Asp Glu
 565 570 575

Ile Cys Pro Gln Leu Tyr Ala Arg Ile Ser Pro Thr Leu Thr Ser His
 580 585 590

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
 Ser Lys Asn Ser Thr Gly Leu Ala Glu Thr Gly Thr His Ser Asn Ser
 595 600 605

Tyr Leu Asp Thr Ser Arg Val Ser Ile Ser Val Leu Val Pro Gly Leu
 610 615 620

Leu Leu Val Phe Val Thr Ser Ala Phe Thr Val Val Gly Met Leu Val
 625 630 635 640

Phe Ile Leu Arg Asn Arg Lys Arg Ser Lys Arg Arg Asp Ala Asn Ser
 645 650 655

Ser Ala Ser Glu Ile Asn Ser Leu Gln Thr Val Cys Asp Ser Ser Tyr
 660 665 670

Trp His Asn Gly Pro Tyr Asn Ala Asp Gly Ala His Arg Val Tyr Asp
 675 680 685

Cys Gly Ser His Ser Leu Ser Asp
 690 695

<210> 92
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 92
 gttgatctg ggcaacaata ac 22

<210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 93
 attgttgtgc aggctgagtt taag 24

<210> 94
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 94
 ggtggctata catgtagtc aattacctgg acacgctgtc ccggg 45

<210> 95
 <211> 2226
 <212> DNA
 <213> Homo sapiens

<400> 95

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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agtcgactgc gtcccttgta cccggcgcca gctgtgttcc tgaccccaga ataactcagg 60
gctgcaccgg gcctggcagc gctccgcaca catttcctgt cgcggcctaa gggaaaactgt 120
tggccgctgg gcccgcgggg ggattcttgg cagttggggg gtccgctcggg agcgagggcg 180
gagggggaagg gagggggaac cgggttgggg aagccagctg tagagggcgg tgaccgcgct 240
ccagacacag ctctgcgtcc tcgagcggga cagatccaag ttgggagcag ctctgcgtgc 300
ggggcctcag agaattgagg cggcggttcgc cctgtgcctc ctctggcagg cgctctggcc 360
cgggcccggg ggcggcgaac accccactgc cgaccgtgct ggctgctcgg cctcgggggc 420
ctgctacagc ctgcaccacg ctaccatgaa gcggcaggcg gccgaggagg cctgcatcct 480
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ctcctgcacc gcgcggagat gcgcggtagt ccagggcacc ggtggggctg agcccgagg 780
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cgagagctc cctaactgcc tagacgactt gggaggcttt gcctgcgaat gtgctacggg 1140
cttcgagctg ggggaaggag gccgctcttg tgtgaccagt ggggaaggac agccgaccct 1200
tggggggacc ggggtgcccc ccaggcgccc gccggccact gcaaccagcc ccgtgccgca 1260
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tgccgtggtc ttcataattg tgagcacagc agtagtagtg ttggtgatct tgaccatgac 1560
agtactgggg cttgtcaagc tctgcttca cgaaagcccc tcttcccagc caaggaagga 1620
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tgggcactcc tgtgaacagt ttttcaactt tgatgaaacg gggaaaccaag aggaacttac 1860
ttgtgtaact gacaatttct gcagaaatcc cccttccctt aaattccctt tactccactg 1920
aggagctaaa tcagaactgc acactccttc cctgatgata gaggaagtgg aagtgccttt 1980
aggatggtga tactggggga ccgggtagtg ctggggagag atattttctt atgtttattc 2040
ggagaatttg gagaagtgat tgaacttttc aagacattgg aaacaaatag aacacaatat 2100
aatttacatt aaaaaataat ttctacaaa atggaaaagga aatgttctat gttgttcagg 2160
ctaggagtat attggttcga aatcccaggg aaaaaataa aaataaaaaa ttaaaggatt 2220
gttgat

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<210> 96
 <211> 490
 <212> PRT
 <213> Homo sapiens

<400> 96
 Met Arg Pro Ala Phe Ala Leu Cys Leu Leu Trp Gln Ala Leu Trp Pro
 1 5 10 15
 Gly Pro Gly Gly Gly Glu His Pro Thr Ala Asp Arg Ala Gly Cys Ser
 20 25 30
 Ala Ser Gly Ala Cys Tyr Ser Leu His His Ala Thr Met Lys Arg Gln
 35 40 45
 Ala Ala Glu Glu Ala Cys Ile Leu Arg Gly Gly Ala Leu Ser Thr Val
 50 55 60
 Arg Ala Gly Ala Glu Leu Arg Ala Val Leu Ala Leu Leu Arg Ala Gly
 65 70 75 80
 Pro Gly Pro Gly Gly Gly Ser Lys Asp Leu Leu Phe Trp Val Ala Leu
 85 90 95

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Glu Arg Arg Arg Ser His Cys Thr Leu Glu Asn Glu Pro Leu Arg Gly
100 105 110

Phe Ser Trp Leu Ser Ser Asp Pro Gly Gly Leu Glu Ser Asp Thr Leu
115 120 125

Gln Trp Val Glu Glu Pro Gln Arg Ser Cys Thr Ala Arg Arg Cys Ala
130 135 140

Val Leu Gln Ala Thr Gly Gly Val Glu Pro Ala Gly Trp Lys Glu Met
145 150 155 160

Arg Cys His Leu Arg Ala Asn Gly Tyr Leu Cys Lys Tyr Gln Phe Glu
165 170 175

Val Leu Cys Pro Ala Pro Arg Pro Gly Ala Ala Ser Asn Leu Ser Tyr
180 185 190

Arg Ala Pro Phe Gln Leu His Ser Ala Ala Leu Asp Phe Ser Pro Pro
195 200 205

Gly Thr Glu Val Ser Ala Leu Cys Arg Gly Gln Leu Pro Ile Ser Val
210 215 220

Thr Cys Ile Ala Asp Glu Ile Gly Ala Arg Trp Asp Lys Leu Ser Gly
225 230 235 240

Asp Val Leu Cys Pro Cys Pro Gly Arg Tyr Leu Arg Ala Gly Lys Cys
245 250 255

Ala Glu Leu Pro Asn Cys Leu Asp Asp Leu Gly Gly Phe Ala Cys Glu
260 265 270

Cys Ala Thr Gly Phe Glu Leu Gly Lys Asp Gly Arg Ser Cys Val Thr
275 280 285

Ser Gly Glu Gly Gln Pro Thr Leu Gly Gly Thr Gly Val Pro Thr Arg
290 295 300

Arg Pro Pro Ala Thr Ala Thr Ser Pro Val Pro Gln Arg Thr Trp Pro
305 310 315 320

Ile Arg Val Asp Glu Lys Leu Gly Glu Thr Pro Leu Val Pro Glu Gln
325 330 335

Asp Asn Ser Val Thr Ser Ile Pro Glu Ile Pro Arg Trp Gly Ser Gln
340 345 350

Ser Thr Met Ser Thr Leu Gln Met Ser Leu Gln Ala Glu Ser Lys Ala
355 360 365

Thr Ile Thr Pro Ser Gly Ser Val Ile Ser Lys Phe Asn Ser Thr Thr
370 375 380

Ser Ser Ala Thr Pro Gln Ala Phe Asp Ser Ser Ser Ala Val Val Phe
385 390 395 400

Ile Phe Val Ser Thr Ala Val Val Val Leu Val Ile Leu Thr Met Thr
405 410 415

Val Leu Gly Leu Val Lys Leu Cys Phe His Glu Ser Pro Ser Ser Gln
420 425 430

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
Pro Arg Lys Glu Ser Met Gly Pro Pro Gly Leu Glu Ser Asp Pro Glu
435 440 445

Pro Ala Ala Leu Gly Ser Ser Ser Ala His Cys Thr Asn Asn Gly Val
450 455 460

Lys val Gly Asp Cys Asp Leu Arg Asp Arg Ala Glu Gly Ala Leu Leu
465 470 475 480

Ala Glu Ser Pro Leu Gly Ser Ser Asp Ala
485 490

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

tggaaggaga tgcgatgccca cctg

24

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

tgaccagtgg ggaaggacag

20

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

acagagcaga ggggtgccttg

20

<213> Artificial Sequence

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

tcagggacaa gtggtgtctc tccc

24

<212> DNA

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 101

tcaggggaagg agtgtgcagt tctg

24

<210> 102

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 102

acagctcccc atctcagtta cttgcatcgc ggacgaaatc ggcgctcgct

50

<210> 103

<211> 2026

<212> DNA

<213> Homo sapiens

<400> 103

| | | | | | | |
|------------|-------------|-------------|-------------|------------|-------------|------|
| cggacgcgtg | ggattcagca | gtggcctgtg | gctgccagag | cagctcctca | ggggaaacta | 60 |
| agcgtcgagt | cagacggcac | cataatcgcc | tttaaaagt | cctccgccct | gccggccgcg | 120 |
| tatcccccg | ctacctgggc | cgccccgcg | cggtgcgcgc | gtgagagggg | gcgcgcgggc | 180 |
| agccgagcgc | cggtgtgagc | cagcgtgtgt | gccagtgtga | gcggcggtgt | gagcgcgggtg | 240 |
| ggtgcggagg | ggcgtgtgtg | ccggcgcgcg | cgccgtgggg | tgcaaacc | gagcgtctac | 300 |
| gctgccatga | ggggcgcgaa | cgcctggg | ccactctgcc | tgctgctggc | tgccgccacc | 360 |
| cagctctcgc | ggcagcagtc | cccagagaga | cctgttttca | catgtggtgg | cattcttact | 420 |
| ggagagtctg | gattttattg | cagtgaaggt | tttccctggag | tgtaccctcc | aaatagcaaa | 480 |
| tgtacttgga | aaatcacagt | tcccgaagga | aaagttagtcg | ttctcaattt | ccgattcata | 540 |
| gacctcgaga | gtgacaacct | gtgccgctat | gactttgtgg | atgtgtacaa | tggccatgcc | 600 |
| aatggccagc | gcattggccg | cttctgtggc | actttccggc | ctggagccct | tgtgtccagt | 660 |
| ggcaacaaga | tgatggtgca | gatgatttct | gatgccaaca | cagctggcaa | tggtttcatg | 720 |
| gccatgttct | ccgctgtctga | accaaaccgaa | agaggggatc | agtattgtgg | aggactcctt | 780 |
| gacagacctt | ccggctcttt | taaaaccccc | aactggccag | accgggatta | ccctgcagga | 840 |
| gtcatttgtg | tgtggcacat | tgtagcccca | aagaatcagc | ttatagaatt | aaagtttgag | 900 |
| aagtttgatg | tggagcgaga | taactactgc | cgatatgatt | atgtggctgt | gtttaatggc | 960 |
| ggggaagtca | acgatgctag | aagaattgga | aagtattgtg | gtgatagtcc | acctgcgcca | 1020 |
| attgtgtctg | agagaaatga | acttcttatt | cagtttttat | cagacttaag | tttaactgca | 1080 |
| gatgggttta | ttggtcacta | catattcagg | ccaaaaaaac | tgcttacaac | tacagaacag | 1140 |
| cctgtcacca | ccacattccc | tgtaccacg | ggtttaaaac | ccaccgtggc | cttgtgtcaa | 1200 |
| caaaagtgtg | gacggacggg | gactctggag | ggcaattatt | gttcaagtga | ctttgtatta | 1260 |
| gccggcactg | ttatcacaac | catcactcgc | gatgggagtt | tgacagccac | agtctcgatc | 1320 |
| atcaacatct | acaaagaggg | aaatttggcg | attcagcagg | cgggcaagaa | catgagtgcc | 1380 |
| aggctgactg | tcgtctgcaa | gcagtgccct | ctcctcagaa | gaggtctaaa | ttacattatt | 1440 |
| atgggccaag | taggtgaaga | tgggcgaggc | aaaatcatgc | caaacagctt | tatcatgatg | 1500 |
| ttcaagacca | agaatcagaa | gctcctggat | gccttaaaaa | ataagcaatg | ttaacagtga | 1560 |
| actgtgtcca | tttaagctgt | attctgccc | tgcttttgaa | agatctatgt | tctctcagta | 1620 |
| gaaaaaaaaa | tacttataaa | attacatatt | ctgaaagagg | attccgaaag | atgggactgg | 1680 |
| ttgactcttc | acatgatgga | ggtatgaggc | ctccgagata | gctgagggaa | gttctttgcc | 1740 |
| tgctgtcaga | ggagcagcta | tctgattgga | aacctgcccga | cttagtgccg | tgataggaag | 1800 |
| ctaaaagtgt | caagcgttga | cagcttggaa | gcgtttattt | atacatctct | gtaaaaggat | 1860 |
| attttagaat | tgagttgtgt | gaagatgtca | aaaaaagatt | ttagaagtgc | aatatttata | 1920 |
| gtgttatttg | tttcacctic | aagcctttgc | cctgaggtgt | tacaatcttg | tcttgcgttt | 1980 |
| tctaaatcaa | tgcttaataa | aatattttta | aaggaaaaaa | aaaaaa | | 2026 |

<210> 104

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 415

<212> PRT

<213> Homo sapiens

<400> 104

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Met Arg Gly Ala Asn Ala Trp Ala Pro Leu Cys Leu Leu Leu Ala Ala
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Ala Thr Gln Leu Ser Arg Gln Gln Ser Pro Glu Arg Pro Val Phe Thr
          20          25          30
Cys Gly Gly Ile Leu Thr Gly Glu Ser Gly Phe Ile Gly Ser Glu Gly
          35          40          45
Phe Pro Gly Val Tyr Pro Pro Asn Ser Lys Cys Thr Trp Lys Ile Thr
          50          55          60
Val Pro Glu Gly Lys Val Val Val Leu Asn Phe Arg Phe Ile Asp Leu
          65          70          75          80
Glu Ser Asp Asn Leu Cys Arg Tyr Asp Phe Val Asp Val Tyr Asn Gly
          85          90          95
His Ala Asn Gly Gln Arg Ile Gly Arg Phe Cys Gly Thr Phe Arg Pro
          100          105          110
Gly Ala Leu Val Ser Ser Gly Asn Lys Met Met Val Gln Met Ile Ser
          115          120          125
Asp Ala Asn Thr Ala Gly Asn Gly Phe Met Ala Met Phe Ser Ala Ala
          130          135          140
Glu Pro Asn Glu Arg Gly Asp Gln Tyr Cys Gly Gly Leu Leu Asp Arg
          145          150          155          160
Pro Ser Gly Ser Phe Lys Thr Pro Asn Trp Pro Asp Arg Asp Tyr Pro
          165          170          175
Ala Gly Val Thr Cys Val Trp His Ile Val Ala Pro Lys Asn Gln Leu
          180          185          190
Ile Glu Leu Lys Phe Glu Lys Phe Asp Val Glu Arg Asp Asn Tyr Cys
          195          200          205
Arg Tyr Asp Tyr Val Ala Val Phe Asn Gly Gly Glu Val Asn Asp Ala
          210          215          220
Arg Arg Ile Gly Lys Tyr Cys Gly Asp Ser Pro Pro Ala Pro Ile Val
          225          230          235          240
Ser Glu Arg Asn Glu Leu Leu Ile Gln Phe Leu Ser Asp Leu Ser Leu
          245          250          255
Thr Ala Asp Gly Phe Ile Gly His Tyr Ile Phe Arg Pro Lys Lys Leu
          260          265          270
Pro Thr Thr Thr Glu Gln Pro Val Thr Thr Thr Phe Pro Val Thr Thr
          275          280          285
Gly Leu Lys Pro Thr Val Ala Leu Cys Gln Gln Lys Cys Arg Arg Thr
          290          295          300
Gly Thr Leu Glu Gly Asn Tyr Cys Ser Ser Asp Phe Val Leu Ala Gly

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CORRECTED SEQUENCE LISTING FROM EPO FILED IN THE U.S. PATENT AND TRADEMARK OFFICE

| | | | |
|-----|-----|-----|-----|
| 305 | 310 | 315 | 320 |
|-----|-----|-----|-----|

CORRECTED SEQUENCE LISTING FROM EPO FILED IN THE U.S. PATENT AND TRADEMARK OFFICE

| | | | |
|-----|-----|-----|-----|
| 305 | 310 | 315 | 320 |
|-----|-----|-----|-----|

Ser Ile Ile Asn Ile Tyr Lys Glu Gly Asn Leu Ala Ile Gln Gln Ala
340 345 350

Gly Lys Asn Met Ser Ala Arg Leu Thr Val Val Cys Lys Gln Cys Pro
355 360 365

Leu Leu Arg Arg Gly Leu Asn Tyr Ile Ile Met Gly Gln Val Gly Glu
370 375 380

Asp Gly Arg Gly Lys Ile Met Pro Asn Ser Phe Ile Met Met Phe Lys
385 390 395 400

Thr Lys Asn Gln Lys Leu Leu Asp Ala Leu Lys Asn Lys Gln Cys
405 410 415

<210> 105

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 105

ccgattcata gacctcgaga gt

22

<210> 106

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 106

gtcaaggagt cctccacaat ac

22

<210> 107

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 107

gtgtacaatg gccatgccaa tggccagcgc attggccgct tctgt

45

<210> 108

| | |
|-------|------|
| <210> | 100 |
| <211> | 1838 |

<212> DNA

<213> Homo sapiens

<400> 108

cggacgcgtg ggcggacgcg tgggcggccc acggcgcccc cgggctgggg cggtcgcttc 60

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ttcctttctcc gtggcctacg aggggtcccca gcctgggtaa agatggccccc atggcccccg 120
aagggcctag tcccagctgt gctctggggc ctcagcctct tcctcaacct cccaggacct 180
atctggctcc agccctctcc acctcccccag tcttctcccc cgctcagcc ccatccgtgt 240
catacctgcc ggggactggg tgacagcttt aacaaggggc tggagagaac catccgggac 300
aacttttgag gtggaaacac tgcctgggag gaagagaatt tgtccaaata caaagacagt 360
gagacccgcc tggtagaggt gctggagggt gtgtgcagca agtcagactt cgagtgccac 420
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tgttcaccac atccccacac cccattggca cttatttatt catctcagga aataaagaaa 1800
ggtccttgaa agttaaaaaa aaaaaaaaaa aaaaaaaa 1838

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<210> 109

<211> 420

<212> PRT

<213> Homo sapiens

<400> 109

Met Ala Pro Trp Pro Lys Gly Leu Val Pro Ala Val Leu Trp Gly
1 5 10 15

Leu Ser Leu Phe Leu Asn Leu Pro Gly Pro Ile Trp Leu Gln Pro Ser
20 25 30

Pro Pro Pro Gln Ser Ser Pro Pro Gln Pro His Pro Cys His Thr
35 40 45

Cys Arg Gly Leu Val Asp Ser Phe Asn Lys Gly Leu Glu Arg Thr Ile
50 55 60

Arg Asp Asn Phe Gly Gly Gly Asn Thr Ala Trp Glu Glu Glu Asn Leu
65 70 75 80

Ser Lys Tyr Lys Asp Ser Glu Thr Arg Leu Val Glu Val Leu Glu Gly
85 90 95

Val Cys Ser Lys Ser Asp Phe Glu Cys His Arg Leu Leu Glu Leu Ser
100 105 110

Glu Glu Leu Val Glu Ser Trp Trp Phe His Lys Gln Gln Glu Ala Pro
115 120 125

Asp Leu Phe Gln Trp Leu Cys Ser Asp Ser Leu Lys Leu Cys Cys Pro
130 135 140

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Gly Thr Phe Gly Pro Ser Cys Leu Pro Cys Pro Gly Gly Thr Glu
145 150 155 160

Arg Pro Cys Gly Gly Tyr Gly Gln Cys Glu Gly Glu Gly Thr Arg Gly
165 170 175

Gly Ser Gly His Cys Asp Cys Gln Ala Gly Tyr Gly Gly Glu Ala Cys
180 185 190

Gly Gln Cys Gly Leu Gly Tyr Phe Glu Ala Glu Arg Asn Ala Ser His
195 200 205

Leu Val Cys Ser Ala Cys Phe Gly Pro Cys Ala Arg Cys Ser Gly Pro
210 215 220

Glu Glu Ser Asn Cys Leu Gln Cys Lys Lys Gly Trp Ala Leu His His
225 230 235 240

Leu Lys Cys Val Asp Ile Asp Glu Cys Gly Thr Glu Gly Ala Asn Cys
245 250 255

Gly Ala Asp Gln Phe Cys Val Asn Thr Glu Gly Ser Tyr Glu Cys Arg
260 265 270

Asp Cys Ala Lys Ala Cys Leu Gly Cys Met Gly Ala Gly Pro Gly Arg
275 280 285

Cys Lys Lys Cys Ser Pro Gly Tyr Gln Gln Val Gly Ser Lys Cys Leu
290 295 300

Asp Val Asp Glu Cys Glu Thr Glu Val Cys Pro Gly Glu Asn Lys Gln
305 310 315 320

Cys Glu Asn Thr Glu Gly Gly Tyr Arg Cys Ile Cys Ala Glu Gly Tyr
325 330 335

Lys Gln Met Glu Gly Ile Cys Val Lys Glu Gln Ile Pro Glu Ser Ala
340 345 350

Gly Phe Phe Ser Glu Met Thr Glu Asp Glu Leu Val Val Leu Gln Gln
355 360 365

Met Phe Phe Gly Ile Ile Ile Cys Ala Leu Ala Thr Leu Ala Ala Lys
370 375 380

Gly Asp Leu Val Phe Thr Ala Ile Phe Ile Gly Ala Val Ala Ala Met
385 390 395 400

Thr Gly Tyr Trp Leu Ser Glu Arg Ser Asp Arg Val Leu Glu Gly Phe
405 410 415

Ile Lys Gly Arg
420

<210> 110

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 110
cctggctatc agcaggtggg ctccaagtgt ctcgatgtgg atgagtgtga 50

<210> 111
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 111
attctgctg aacactgagg gc 22

<210> 112
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 112
atctgcttgt agccctcggc ac 22

<210> 113
<211> 1616
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1461)..(1461)
<223> a, t, c or g

<400> 113
tgagaccctc ctgcagcctt ctcaaggagc agccccactc tgcctcttgc tcctccaggg 60
cagcaccatg cagccccctgt ggctctgctg ggcactctgg gtgttgcccc tggccagccc 120
cggggccgcc ctgaccgggg agcagctcct gggcagcctg ctgcggcagc tgcagctcaa 180
agaggtgccc accctggaca gggccgacat ggaggagctg gtcacccccca cccacgtgag 240
ggcccagtag gtggccctgc tgcagcgcag ccacggggac cgctcccgcg gaaagagggt 300
cagccagagc ttccgagagg tggccggcag gttcctggcg ttggaggcca gcacacacct 360
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gcgcagcgcc cggggccggg tgaccgtcga gtggctgcgc gtccgcgacg acggctccaa 540
ccgcacctcc ctcatcgact ccaggctggt gtccgtccac gagagcggct ggaaggcctt 600
cgacgtgacc gaggccgtga acttctggca gcagctgagc cggccccggc agccgctgct 660
gctacaggtg tcggtgcaga gggagcatct gggcccgcgt gcgtccggcg cccacaagct 720
ggtccgcttt gcctcgcagg gggcgccagc cgggcttggg gagccccagc tggagctgca 780
caccctggac ctttgggact atggagctca gggcgactgt gaccctgaag caccaatgac 840
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cgagaactgg gtgctggagc ccccgggctt cctggcttat gagtgtgtgg gcacctgccg 960
gcagcccccg gaggccctgg ccttcaagtg gccgtttctg gggcctcgac agtgcatcgc 1020
ctcggagact gactcgctgc ccatgatcgt cagcatcaag gaggggaggca ggaccaggcc 1080
ccaggtggtc agcctgcccc acatgagggt gcagaagtgc agctgtgcct cggatggtgc 1140
gctcgtgcca aggaggtccc agccataggc gcctagtgtg gccatcgagg gacttgactt 1200
gtgtgtgttt ctgaagtgtt cgaggggtacc aggagagctg gcgatgactg aactgctgat 1260
ggacaaatgc tctgtgctct ctagttagcc ctgaatttgc ttcctctgac aagttacctc 1320
acctaatttt tgcttctcag gaatgagaat ctttgggcac tggagagccc ttgctcagtt 1380
ttctctattc ttattattca ctgcactata ttctaagcac ttacatgtgg agatactgta 1440

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
acctgagggc agaaagccca ntgtgtcatt gtttacttgt cctgtcactg gatctgggct 1500
aaagtctctc accaccactc tggacctaaag acctgggggt aagtgtgggt tgtgcatccc 1560
caatccagat aataaagact ttgtaaaaca tgaataaaac acatttttatt ctaaaa 1616

<210> 114
<211> 366
<212> PRT
<213> Homo sapiens

<400> 114
Met Gln Pro Leu Trp Leu Cys Trp Ala Leu Trp Val Leu Pro Leu Ala
1 5 10 15
Ser Pro Gly Ala Ala Leu Thr Gly Glu Gln Leu Leu Gly Ser Leu Leu
20 25 30
Arg Gln Leu Gln Leu Lys Glu Val Pro Thr Leu Asp Arg Ala Asp Met
35 40 45
Glu Glu Leu Val Ile Pro Thr His Val Arg Ala Gln Tyr Val Ala Leu
50 55 60
Leu Gln Arg Ser His Gly Asp Arg Ser Arg Gly Lys Arg Phe Ser Gln
65 70 75 80
Ser Phe Arg Glu Val Ala Gly Arg Phe Leu Ala Leu Glu Ala Ser Thr
85 90 95
His Leu Leu Val Phe Gly Met Glu Gln Arg Leu Pro Pro Asn Ser Glu
100 105 110
Leu Val Gln Ala Val Leu Arg Leu Phe Gln Glu Pro Val Pro Lys Ala
115 120 125
Ala Leu His Arg His Gly Arg Leu Ser Pro Arg Ser Ala Arg Ala Arg
130 135 140
Val Thr Val Glu Trp Leu Arg Val Arg Asp Asp Gly Ser Asn Arg Thr
145 150 155 160
Ser Leu Ile Asp Ser Arg Leu Val Ser Val His Glu Ser Gly Trp Lys
165 170 175
Ala Phe Asp Val Thr Glu Ala Val Asn Phe Trp Gln Gln Leu Ser Arg
180 185 190
Pro Arg Gln Pro Leu Leu Leu Gln Val Ser Val Gln Arg Glu His Leu
195 200 205
Gly Pro Leu Ala Ser Gly Ala His Lys Leu Val Arg Phe Ala Ser Gln
210 215 220
Gly Ala Pro Ala Gly Leu Gly Glu Pro Gln Leu Glu Leu His Thr Leu
225 230 235 240
Asp Leu Gly Asp Tyr Gly Ala Gln Gly Asp Cys Asp Pro Glu Ala Pro
245 250 255
Met Thr Glu Gly Thr Arg Cys Cys Arg Gln Glu Met Tyr Ile Asp Leu
260 265 270
Gln Gly Met Lys Trp Ala Glu Asn Trp Val Leu Glu Pro Pro Gly Phe
275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Ala Tyr Glu Cys Val Gly Thr Cys Arg Gln Pro Pro Glu Ala Leu
290 295 300

Ala Phe Lys Trp Pro Phe Leu Gly Pro Arg Gln Cys Ile Ala Ser Glu
305 310 315 320

Thr Asp Ser Leu Pro Met Ile Val Ser Ile Lys Glu Gly Gly Arg Thr
325 330 335

Arg Pro Gln Val Val Ser Leu Pro Asn Met Arg Val Gln Lys Cys Ser
340 345 350

Cys Ala Ser Asp Gly Ala Leu Val Pro Arg Arg Leu Gln Pro
355 360 365

<210> 115

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 115

aggactgccca taacttgctt g

21

<210> 116

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 116

ataggagttg aagcagcgct gc

22

<210> 117

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial sequence: Synthetic
oligonucleotide probe

<400> 117

tgtgtggaca tagacgagtg ccgctaccgc tactgccagc accgc

45

<210> 118

<211> 1857

<212> DNA

<213> Homo sapiens

<400> 118

gtctgttccc aggagtcctt cggcggctgt tgtgtcagtg gcctgatcgc gatggggaca 60
aaggcgcaag tcgagaggaa actgttgtgc ctcttcatat tggcgatcct gttgtgctcc 120
ctggcattgg gcagtgttac agtgcactct tctgaacctg aagtcagaat tcctgagaat 180
aatcctgtga agttgtcctg tgcctactcg ggcttttctt ctccccgtgt ggagtgggaag 240

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tttgaccaag gagacaccac cagactcgtt tgctataata acaagatcac agcttcctat 300
gaggaccggg tgaccttctt gccactggt atcaccttca agtccgtgac acgggaagac 360
actgggacat acacttgtat ggtctctgag gaaggcggca acagctatgg ggaggtcaag 420
gtcaagctca tcgtgcttgt gacctccatcc aagcctacag ttaacatccc ctccctcgcc 480
accattggga accgggcagt gctgacatgc tcagaacaag atgggtccccc accttctgaa 540
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ggagaaaccc tactggaaat acaaagttag ccaggcatgg tggtgcatgc ctgtagtccc 1800
agctgctcag gagcctggca acaagagcaa aactccagct caaaaaaaaa aaaaaaa 1857

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<210> 119
 <211> 299
 <212> PRT
 <213> Homo sapiens

<400> 119
 Met Gly Thr Lys Ala Gln Val Glu Arg Lys Leu Leu Cys Leu Phe Ile
 1 5 10 15
 Leu Ala Ile Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
 20 25 30
 Ser Ser Glu Pro Glu Val Arg Ile Pro Glu Asn Asn Pro Val Lys Leu
 35 40 45
 Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
 50 55 60
 Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr
 65 70 75 80
 Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
 85 90 95
 Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser
 100 105 110
 Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val
 115 120 125
 Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr
 130 135 140
 Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro
 145 150 155 160

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn
165 170 175
Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro
180 185 190
Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly
195 200 205
Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser
210 215 220
Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val
225 230 235 240
Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly
245 250 255
Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly
260 265 270
Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu
275 280 285
Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val
290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial sequence: Synthetic
oligonucleotide probe

<400> 120

tcgcggagct gtgttctggt tccc

24

<210> 121

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial sequence: Synthetic
oligonucleotide probe

<400> 121

tgatcgcgat ggggacaaag gcgcaagctc gagaggaaac tgttgtgcct

50

<210> 122

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial sequence: Synthetic
oligonucleotide probe

<400> 122

acacctggtt caaagatggg

20

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 123
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 123
 taggaagagt tgctgaaggc acgg 24

<210> 124
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 124
 ttgccttact caggtgctac 20

<210> 125
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 125
 actcagcagt ggtaggaaag 20

<210> 126
 <211> 1210
 <212> DNA
 <213> Homo sapiens

<400> 126
 cagcgcgtgg ccggcgccgc tgtgggggaca gcatgagcgg cggttggatg gcgcaggttg 60
 gagcgtggcg aacaggggct ctgggccttg cgctgctgct gctgctcggc ctcggactag 120
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 agctaggatg gggaaacctg cacagccaga actgaggggc tggccccagg cagctcccag 1140
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aagttgcttc

<210> 127
<211> 282
<212> PRT
<213> Homo sapiens

<400> 127

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Met Ser Gly Gly Trp Met Ala Gln Val Gly Ala Trp Arg Thr Gly Ala
 1           5           10           15
Leu Gly Leu Ala Leu Leu Leu Leu Gly Leu Gly Leu Gly Leu Glu
          20           25           30
Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
 35           40           45
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
 50           55           60
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
 65           70           75           80
Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
          85           90           95
Lys Gly Gln Cys Pro Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
          100          105          110
Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser
          115          120          125
Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp
          130          135          140
Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp
          145          150          155          160
Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly
          165          170          175
Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser
          180          185          190
Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val
          195          200          205
Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly
          210          215          220
Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Val Leu Ser Ala
          225          230          235          240
Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln
          245          250          255
Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu
          260          265          270
Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro
          275          280

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<210> 128

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 128
aagttccagt gccgcaccag tggc                                24

<210> 129
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 129
ttggttcac agccgagctc gtcg                                24

<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 130
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc    50

<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1837)..(1837)
<223> a, t, c or g

<400> 131
cccacgcgtc cgggtctcgtc cgctcgcgca gcggcggcag cagaggtcgc gcacagatgc 60
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cagactcttg caagctggat gccctctgtg gatgaaagat gtatcatgga atgaaccaga 180
gcaatggaga tggatttcta gagcagcagc agcagcagca gcaacctcag tccccccaga 240
gactcttggc cgtgatcctg tggtttcagc tggcgctgtg cttcggccct gcacagctca 300
cgggcggggt cgatgacctt caagtgtgtg ctgaccccg g cattcccag aatggcttca 360
ggacccccag cggagggggt ttctttgaag gctctgtagc ccgatttcac tgccaagacg 420
gattcaagct gaagggcgct acaaagagac tgtgtttgaa gcattttaat ggaaccctag 480
gctggatccc aagtgataat tccatctgtg tgcaagaaga ttgccgtatc cctcaaatacg 540
aagatgctga gattcataac aagacatata gacatggaga gaagctaata atcacttgct 600
atgaaggatt caagatccgg taccgagacc tacacaatat ggtttcatta tgtcgcgatg 660
atggaacgtg gaataatctg cccatctgtc aaggctgcct gagacctcta gcctcttcta 720
atggctatgt aaacatctct gagctccaga cctccttccc ggtggggact gtgatctcct 780
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ctccaatggt gagtacagga gatttcgtct gccaccccg gccttgtag cgctacaacc 960
acggaactgt ggtggagttt tactgcgata ctggctacag cctcaccagc gactacaagt 1020

```


CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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acatcacctg ccagtatgga gagtggtttc cttcttatca agtctactgc atcaaatcag 1080
agcaaactg gcccagcacc catgagaccc tcctgaccac gtggaagatt gtggcggtca 1140
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```

<210> 132

<211> 490

<212> PRT

<213> Homo sapiens

<400> 132

Met Tyr His Gly Met Asn Pro Ser Asn Gly Asp Gly Phe Leu Glu Gln
1 5 10 15

Gln Gln Gln Gln Gln Gln Pro Gln Ser Pro Gln Arg Leu Leu Ala Val
20 25 30

Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr
35 40 45

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu
50 55 60

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val
65 70 75 80

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys
85 90 95

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser
100 105 110

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu
115 120 125

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile
130 135 140

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn
145 150 155 160

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile
165 170 175

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn
180 185 190

Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr
195 200 205

Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys
210 215 220

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu
 225 230 235 240
 Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe
 245 250 255
 Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val
 260 265 270
 Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr
 275 280 285
 Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys
 290 295 300
 Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr
 305 310 315 320
 Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu
 325 330 335
 Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His
 340 345 350
 Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe
 355 360 365
 Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala
 370 375 380
 Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val
 385 390 395 400
 Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr
 405 410 415
 Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys
 420 425 430
 Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro
 435 440 445
 Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile
 450 455 460
 Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His
 465 470 475 480
 His Ala His Trp Val Leu Phe Leu Arg Asn
 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 133

atctcctatc gctgctttcc cgg

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 134
 <211> 23
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 134
 agccaggatc gcagtaaaac tcc 23

<210> 135
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 135
 atttaaactt gatgggtctg cgtatcttga gtgcttacaa aaccttatct 50

<210> 136
 <211> 1815
 <212> DNA
 <213> Homo sapiens

<400> 136
 cccacgcgtc cgctccgcgc cctccccccc gcctcccgtg cgggtccgtcg gtggcctaga 60
 gatgctgctg ccgcggttgc agttgtcgcg cacgcctctg cccgccagcc cgctccaccg 120
 ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgggc catgaggccg ggaaccgcgc 180
 tacaggccgt gctgctggcc gtgctgctgg tggggctgcg ggccgcgacg ggtcgctgc 240
 tgagtgcctc ggatttggac ctgagaggag ggcagccagt ctgccgggga gggacacaga 300
 ggccttgcta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
 ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
 agaaactgat agaaaagtgc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
 ggctcaggag gcgtgaggag aaacaaagca atagcacagc ctgccaggac ctttatgctt 540
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 ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
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 tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaatgg 1260
 ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tgggtattag gacatataaa 1320
 aaactgaaac tgacaacaat ggaaaagaaa tgataagcaa aatcctctta ttttctataa 1380
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 tccagctcga ccttatgaga aggtaccttg ccaggtctg gcacatagta gagtctcaat 1560
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 aaagatgggc tgtggagctt ggaaaaccac ctctgttttc cttgctctat acagcagcac 1680
 atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
 ttggcctgtg catcggcaat tctcatatct gtttttttca aagaataaaa tcaaataaag 1800
 agcaggaaaa aaaaa 1815

<210> 137

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 382

<212> PRT

<213> Homo sapiens

<400> 137

```

Met Arg Pro Gly Thr Ala Leu Gln Ala Val Leu Leu Ala Val Leu Leu
 1          5          10          15
Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu
          20          25          30
Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro
          35          40          45
Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe
          50          55          60
Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser
          65          70          75          80
Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn
          85          90          95
Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Arg Glu
          100          105          110
Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr
          115          120          125
Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser
          130          135          140
Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro
          145          150          155          160
Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys
          165          170          175
Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala
          180          185          190
Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro
          195          200          205
Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys
          210          215          220
Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser
          225          230          235          240
Ile Pro Leu Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val
          245          250          255
Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys
          260          265          270
Lys Gln His Thr Ile Trp Pro Ser Pro His Gln Gly Asn Ser Pro Asp
          275          280          285
Leu Glu Val Tyr Asn Val Ile Arg Lys Gln Ser Glu Ala Asp Leu Ala
          290          295          300
Glu Thr Arg Pro Asp Leu Lys Asn Ile Ser Phe Arg Val Cys Ser Gly

```

305 310 315 320

Glu Ala Thr Pro Asp Asp Met Ser Cys Asp Tyr Asp Asn Met Ala Val
325 330 335

Asn Pro Ser Glu Ser Gly Phe Val Thr Leu Val Ser Val Glu Ser Gly
340 345 350

Phe Val Thr Asn Asp Ile Tyr Glu Phe Ser Pro Asp Gln Met Gly Arg
355 360 365

Ser Lys Glu Ser Gly Trp Val Glu Asn Glu Ile Tyr Gly Tyr
370 375 380

<210> 138
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 138
gttcattgaa aacctcttgc catctgatgg tgacttctgg attgggctca 50

<210> 139
<211> 24
<212> DNA
<213> Artificial sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 139
aagccaaaga agcctgcagg aggg 24

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<210> 140
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 140
cagtccaagc ataaagggtcc tggc 24

```
<210> 141
<211> 1514
<212> DNA
<213> Homo sapiens
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| | | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|--|
| <400> | 141 | | | | | | |
| gggggtctccc | tcagggcccg | gaggcacagc | ggtccctgct | tgctgaaggg | ctggatgtac | 60 | |
| gcatccgcag | gttcccgcg | acttgggggc | gcccgctgag | ccccggcgcc | cgcagaagac | 120 | |
| ttgtgtttgc | ctcctgcagc | ctcaaccccg | agggcagcga | gggcctacca | ccatgatcac | 180 | |
| tggtgtgttc | agcatgcgct | tgtggacccc | agtgggcgct | ctgacctcgc | tggcgtactg | 240 | |
| ccctgcaccag | cggcggtg | ccctggccga | gctgcaggag | gccgatggcc | agtgtccggt | 300 | |
| cgaccgcagc | ctgctgaagt | tgaaaatggt | gcaggtcgtg | tttcgacacg | gggctcggag | 360 | |
| tcctctcaag | ccgctcccgc | tggaggagca | ggtagagtgg | aacccccagc | tattagaggt | 420 | |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

```

cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
gctgaccaag gtgggcatgc agcaaagtgt tgccttgagg gagagactga ggaagaacta 600
tgtggaagac attccctttc ttccaccaac cttcaaccca caggaggtct ttattcgttc 660
cactaacatt ttctggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagt 720
tcagaaagaa ggacccatca tcatccacac tgatgaagca gattcagaag tcttgatatcc 780
caactaccaa agctgctgga gcctgaggca gagaaccaga ggccggaggc agactgcctc 840
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gaccctgggg atttttgacc acaaattggc accgtttgct gttgacctga ccatggaact 1260
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gcctttatac aatg 1514

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<210> 142
 <211> 428
 <212> PRT
 <213> Homo sapiens

<400> 142
 Met Ile Thr Gly Val Phe Ser Met Arg Leu Trp Thr Pro Val Gly Val
 1 5 10 15
 Leu Thr Ser Leu Ala Tyr Cys Leu His Gln Arg Arg Val Ala Leu Ala
 20 25 30
 Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
 35 40 45
 Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
 50 55 60
 Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
 65 70 75 80
 Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
 85 90 95
 Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu
 100 105 110
 Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly
 115 120 125
 Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val
 130 135 140
 Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe
 145 150 155 160
 Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu
 165 170 175
 Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile Ile His
 180 185 190
 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

195 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu
210 215 220

Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly
225 230 235 240

Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val
245 250 255

Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg
260 265 270

Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile
275 280 285

Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe
290 295 300

Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr
305 310 315 320

Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val
325 330 335

Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp
340 345 350

Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu
355 360 365

Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val
370 375 380

Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn
385 390 395 400

Ala Met Ser Val Tyr Thr Leu Ser Pro Glu Lys Tyr His Ala Leu Cys
405 410 415

Ser Gln Thr Gln Val Met Glu Val Gly Asn Glu Glu
420 425

<210> 143

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 143

ccaactacca aagctgctgg agcc

24

<210> 144

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Page 71

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
oligonucleotide probe

<400> 144
gcagctctat taccacggga agga

24

<210> 145
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 145
tccttcccgt ggtaatagag ctgc

24

<210> 146
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 146
ggcagagaac cagaggccgg aggagactgc ctctttacag ccagg

45

<210> 147
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 147
ctcctcttaa catacttgca gctaaaacta aatattgctg cttggggacc tccttctagc 60
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caaccatgat gaagacacgt gggtcgaatg tgaagatccc tttgacttga gactagtagg 840
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acggaatttt aaggataaat tttctgaatt ggttatgggg tttctgaaat tggctctata 1620
atctaattag atataaaatt ctggttaact tatttacaat aataaagata gcactatgtg 1680

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
1686

ttcaaa

<210> 148
<211> 347
<212> PRT
<213> Homo sapiens

<400> 148
Met Ala Leu Leu Phe Ser Leu Ile Leu Ala Ile Cys Thr Arg Pro Gly
1 5 10 15
Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
20 25 30
Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
35 40 45
Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
50 55 60
Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
65 70 75 80
Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys
85 90 95
Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr
100 105 110
Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu
115 120 125
Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro
130 135 140
Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr
145 150 155 160
Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys
165 170 175
Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn
180 185 190
Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys
195 200 205
Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly
210 215 220
Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp
225 230 235 240
Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg
245 250 255
Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn
260 265 270
Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly
275 280 285
Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

290

295

300

Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln
 305 310 315 320

Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr
 325 330 335

His Gln Glu Asp Val Ala Val Ile Cys Ser Val
 340 345

<210> 149

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 149

ttcagctcat caccttcacc tgcc

24

<210> 150

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 150

ggctcataca aaataccact aggg

24

<210> 151

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 151

gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt

50

<210> 152

<211> 1427

<212> DNA

<213> Homo sapiens

<400> 152

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 gaagggtgaag gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180
 cctgggcgctc ttcggcctct tccggctgct gcagtggtg cgcggaagg cctacctgct 240
 gaatgctgtg gtggtgatca caggcgccac ctcagggtg ggcaaagaat gtgcaaaagt 300
 cttctatgct gcgggtgcta aactggtgct ctgtggccgg aatggtgggg ccctagaaga 360
 gctcatcaga gaacttaccg cttctcatgc caccaagggt cagacacaca agccttactt 420
 ggtgaccttc gacctcacag actctggggc catagttgca gcagcagctg agatcctgca 480
 gtgctttggc tatgtcgaca tacttgtaaa caatgctggg atcagctacc gtggtaccat 540
 catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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tgctctaacg aaagcactcc tgccctccat gatcaagagg aggcaaggcc acattgtcgc 660
catcagcagc atccagggca agatgagcat tccttttcga tcagcatatg cagcctccaa 720
gcacgcaacc caggctttct ttgactgtct gcggtgccgag atggaacagt atgaaattga 780
ggtgaccgtc atcagccccg gctacatcca caccaacctc tctgtaaagc ccatcaccgc 840
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agggccaggg cagagaagca gcactcttag gcttgcttac tctacaaggg acagttgcat 1140
ttgttgagac tttaatggag atttgtctca caagtgggaa agactgaaga aacacatctc 1200
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tctcaaacag taaaaaaaaa aaaaaagggc ggccgcgact ctagagtcga cctgcagaag 1380
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<210> 153

<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

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Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
 1             5             10             15
Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
          20             25             30
Ala Tyr Leu Arg Asn Ala Val Val Ile Thr Gly Ala Thr Ser Gly
          35             40             45
Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
          50             55             60
Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
          65             70             75             80
Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
          85             90             95
Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
          100            105            110
Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
          115            120            125
Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
          130            135            140
Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
          145            150            155            160
Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
          165            170            175
Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
          180            185            190
Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
          195            200            205
Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr
          210            215            220

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
225 230 235 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val
260 265 270

Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Ala Ser Arg Ala Arg Lys Glu
290 295 300

Arg Lys Ser Lys Asn Ser
305 310

<210> 154

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 154

ggtgctaaac tgggtgctctg tggc

24

<210> 155

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 155

cagggcaaga tgagcattcc

20

<210> 156

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 156

tcatactggt ccatctcggc acgc

24

<210> 157

<211> 50

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 157
aatggtgggg ccctagaaga gctcatcaga gaactcaccg cttctcatgc 50

<210> 158
<211> 1771
<212> DNA
<213> Homo sapiens

<400> 158
cccacgcgtc cgctgggtgtt agatcgagca accctctaaa agcagtttag agtggtaaaa 60
aaaaaaaaaa acacacccaaa cgctcgagc cacaaaaggg atgaaatttc ttctggacat 120
cctcctgctt ctcccgttac tgatcgctcg ctccctagag tccttcgtga agctttttat 180
tcctaagagg agaaaatcag tcaccggcga aatcggtgctg attacaggag ctgggcatgg 240
aattgggaga ctgactgcct atgaatttgc taaacttaaa agcaagctgg ttctctggga 300
tataaataag catggactgg aggaaacagc tgccaaatgc aagggactgg gtgccaaagg 360
tcataccttt gtggttagact gcagcaaccg agaagataat tacagctctg caaagaagg 420
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<210> 159
<211> 300
<212> PRT
<213> Homo sapiens

<400> 159
Met Lys Phe Leu Leu Asp Ile Leu Leu Leu Leu Pro Leu Leu Ile Val
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Cys Ser Leu Glu Ser Phe Val Lys Leu Phe Ile Pro Lys Arg Arg Lys
20 25 30
Ser Val Thr Gly Glu Ile Val Leu Ile Thr Gly Ala Gly His Gly Ile
35 40 45
Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
50 55 60
Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys
65 70 75 80
Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn
85 90 95

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp
115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn
130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr
145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His
165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala
180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile
195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly
210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu
225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met
245 250 255

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile
260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys
275 280 285

Phe Asp Ala Val Ile Gly Tyr Lys Met Lys Ala Gln
290 295 300

<210> 160

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 160

ggtgaaggca gaaattggag atg

23

<210> 161

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 161

atcccatgca tcagcctgtt tacc

24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 162
 <211> 48
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 162
 gctggtgtag tctatacatc agatttggtt gctacacaag atcctcag 48

<210> 163
 <211> 2076
 <212> DNA
 <213> Homo sapiens

<400> 163
 cccacgcgtc cgccggacgcg tgggtcgact agttctagat cgcgagcggc cgcccgcggc 60
 tcagggagga gcaccgactg cgccgcaccc tgagagatgg ttggtgccat gtggaagggtg 120
 attgtttcgc tggctctggt gatgcctggc ccctgtgatg ggctgtttcg ctccctatac 180
 agaagtgttt ccatgccacc taaggagagc tcaggacagc cattattttct cacccttac 240
 attgaagctg ggaagatcca aaaaggaaga gaattgagtt tggctcggccc tttcccagga 300
 ctgaacatga agagttatgc cggcttcctc accgtgaata agacttaca cagcaacctc 360
 ttcttctggt tcttcccagc tcagatacag ccagaagatg cccagtagt tctctggcta 420
 caggggtgggc cgggagggtt atccatgttt ggactccttg tggaacatgg gccttatgtt 480
 gtcacaagta acatgacctt gcgtgacaga gacttcccct ggaccacaac gctctccatg 540
 ctttacattg acaatccagt gggcacaggc ttcagtttta ctgatgatac ccacggatat 600
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 gtgtttggaa atattatttg ataagaatag ctcaattatc ccaaataaat ggatgaagct 1980
 ataatagttt tggggaaaag atttcaaat gtataaagtc ttagaacaaa agaattcttt 2040
 gaaataaaaa tattatatat aaaagtaaaa aaaaaa 2076

<210> 164
 <211> 476
 <212> PRT
 <213> Homo sapiens

<400> 164
 Met Val Gly Ala Met Trp Lys Val Ile Val Ser Leu Val Leu Leu Met
 1 5 10 15

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Pro Gly Pro Cys Asp Gly Leu Phe Arg Ser Leu Tyr Arg Ser Val Ser
20 25 30
Met Pro Pro Lys Gly Asp Ser Gly Gln Pro Leu Phe Leu Thr Pro Tyr
35 40 45
Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
50 55 60
Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val
65 70 75 80
Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
85 90 95
Ile Gln Pro Glu Asp Ala Pro Val Val Leu Trp Leu Gln Gly Gly Pro
100 105 110
Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
115 120 125
Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
130 135 140
Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
145 150 155 160
Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
165 170 175
Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
180 185 190
Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
195 200 205
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
210 215 220
Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser
225 230 235 240
Asp Pro Glu Ser Ile Ile Gly Gly Tyr Ala Glu Phe Leu Tyr Gln Ile
245 250 255
Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
260 265 270
Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu
275 280 285
Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr
290 295 300
Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys
305 310 315 320
Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro
325 330 335
Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly
340 345 350

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys
 355 360 365
 Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn
 370 375 380
 Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu
 385 390 395 400
 Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys
 405 410 415
 Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile
 420 425 430
 Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly Gly His
 435 440 445
 Ile Leu Pro Tyr Asp Gln Pro Leu Arg Ala Phe Asp Met Ile Asn Arg
 450 455 460
 Phe Ile Tyr Gly Lys Gly Trp Asp Pro Tyr Val Gly
 465 470 475

<210> 165

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 165

ttccatgcca cctaaggag actc

24

<210> 166

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 166

tggatgaggt gtgcaatggc tggc

24

<210> 167

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 167

agctctcaga ggctggtcat aggg

24

<210> 168

<211> 50

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 168

gtcggccctt tcccaggact gaacatgaag agttatgccg gcttcctcac

50

<210> 169

<211> 2477

<212> DNA

<213> Homo sapiens

<400> 169

| | | | | | | |
|------------|-------------|-------------|------------|-------------|-------------|------|
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| atttttccct | ttcctaacaa | gttctaacag | ctgttctaac | agctagtgat | caggggttct | 120 |
| tcttgctgga | gaagaaaggg | ctgagggcag | agcagggcac | tctcactcag | ggtgaccagc | 180 |
| tccttgcttc | tctgtggata | acagagcatg | agaaagtga | gagatgcagc | ggagtggagt | 240 |
| gatggaagtc | taaaatagga | aggaattttg | tgtgcaatat | cagactcttg | gagcagttga | 300 |
| cctggagagc | ctgggggagg | gcctgcctaa | caagctttca | aaaaacagga | gcgacttcca | 360 |
| ctgggctggg | ataagacgtg | ccggtaggat | agggagagct | gggttttagtc | ctaatatcaa | 420 |
| attgactggc | tgggtgaact | tcaacagcct | tttaacctct | ctgggagatg | aaaacgatgg | 480 |
| cttaaggggc | cagaaataga | gatgctttgt | aaaataaaat | tttaaaaaaa | gcaagtattt | 540 |
| tatagcataa | aggctagaga | ccaaaataga | taacaggatt | ccctgaacat | tcctaagagg | 600 |
| gagaaagtat | gttaaaaaata | gaaaaaccaa | aatgcagaag | gaggagactc | acagagctaa | 660 |
| accaggatgg | ggaccctggg | tcaggccagc | ctctttgctc | ctcccggaaa | ttatttttgg | 720 |
| tctgaccact | ctgccttggt | ttttgcagaa | tcattgtgag | gccaaaccgg | gaaggtggag | 780 |
| cagatgagca | cacacaggag | ccgtctcctc | accgccggcc | ctctcagcat | ggaacagagg | 840 |
| cagccctggc | cccgggccct | ggagggtggac | agccgctctg | tggctcctgt | ctcagtgggt | 900 |
| tgggtgctgc | tggccccccc | agcagccggc | atgcctcagt | tcagcacctt | ccactctgag | 960 |
| aatcgtgact | ggaccttcaa | ccacttgacc | gtccaccaag | ggacgggggc | cgctctatgt | 1020 |
| ggggccatca | accgggtcta | taagctgaca | ggcaacctga | ccatccagggt | ggctcataag | 1080 |
| acaggggcag | aagaggacaa | caagtctcgt | taccggcccc | tcattcgtgca | gccctgcagc | 1140 |
| gaagtgtcta | ccctcaccac | caatgtcaac | aagctgtcca | tcattgacta | ctctgagaac | 1200 |
| gccttgctgg | cctgtgggag | cctctaccag | gggtctgca | agctgctgca | gctggatgac | 1260 |
| ctcttcattc | tgggtggagcc | atcccacaag | aaggagcact | acctgtccag | tgtcaacaag | 1320 |
| acgggcacca | tgtacggggt | gattgtgctc | tctgaggggt | aggatggcaa | gctcttcatt | 1380 |
| ggcacggctg | tggatgggaa | gcaggattac | ttcccgaacc | tgtccagccg | gaagctgccc | 1440 |
| cgagaccctg | agtcctcagc | catgctcgac | tatgagctac | acagcgattt | tgtctcctct | 1500 |
| ctcatcaaga | tcccttcaga | caccctggcc | ctggctctcc | actttgacat | cttctacatc | 1560 |
| tacggctttg | ctagtggggg | ctttgtctac | tttctcactg | tccagcccga | gacccctgag | 1620 |
| ggtgtggcca | tcaactccgc | tggagacctc | ttctacacct | cacgcattct | gcggctctgc | 1680 |
| aaggatgacc | ccaagtcca | ctcatagctg | tccctgacct | tcggctgcac | ccgggcccgg | 1740 |
| gtggaatacc | gcctcctgca | ggctgcttac | ctggccaagc | ctggggactc | actggcccag | 1800 |
| gccttcaata | tcaccagcca | ggacgatgta | ctctttgcca | tcttctccaa | agggcagaag | 1860 |
| cagtatcacc | acccgcccga | tgactctgcc | ctgtgtgcct | tccctatccg | ggccatcaac | 1920 |
| ttgcagatca | aggagcgctt | gcagtctctg | taccagggcg | agggcaacct | ggagctcaac | 1980 |
| tggctgctgg | ggaaggacgt | ccagtgcacg | aaggcgcttg | tccccatcga | tgataacttc | 2040 |
| tgtggactgg | acatcaacca | gcccctggga | ggctcaactc | cagtggaggg | cctgaccctg | 2100 |
| tacaccacca | gcaggggacc | catgacctct | gtggcctcct | acgtttacaa | cggctacagc | 2160 |
| gtggtttttg | tggggactaa | gagtggaag | ctgaaaaagg | taagagtcta | tgagttcaga | 2220 |
| tgtctcaatg | ccattcacct | cctcagcaaa | gagtcctctt | tgggaaggtag | ctattgggtg | 2280 |
| agatttaact | ataggcaact | ttattttctt | ggggaacaaa | ggtgaaatgg | ggaggtaaga | 2340 |
| aggggttaat | tttgtgactt | agcttctagc | tacttctctc | agccatcagt | cattgggtat | 2400 |
| gtaaggaatg | caagcgtatt | tcaatatttc | ccaaacttta | agaaaaaact | ttaagaagggt | 2460 |
| acatctgcaa | aagcaaaa | | | | | 2477 |

<210> 170

<211> 552

<212> PRT

<213> Homo sapiens

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 170

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Met Gly Thr Leu Gly Gln Ala Ser Leu Phe Ala Pro Pro Gly Asn Tyr
 1           5           10           15
Phe Trp Ser Asp His Ser Ala Leu Cys Phe Ala Glu Ser Cys Glu Gly
          20           25           30
Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
      35           40           45
Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
 50           55           60
Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
 65           70           75           80
Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His
          85           90           95
Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly
          100          105          110
Thr Gly Ala Val Tyr Val Gly Ala Ile Asn Arg Val Tyr Lys Leu Thr
      115          120          125
Gly Asn Leu Thr Ile Gln Val Ala His Lys Thr Gly Pro Glu Glu Asp
      130          135          140
Asn Lys Ser Arg Tyr Pro Pro Leu Ile Val Gln Pro Cys Ser Glu Val
      145          150          155          160
Leu Thr Leu Thr Asn Asn Val Asn Lys Leu Leu Ile Ile Asp Tyr Ser
          165          170          175
Glu Asn Arg Leu Leu Ala Cys Gly Ser Leu Tyr Gln Gly Val Cys Lys
          180          185          190
Leu Leu Arg Leu Asp Asp Leu Phe Ile Leu Val Glu Pro Ser His Lys
          195          200          205
Lys Glu His Tyr Leu Ser Ser Val Asn Lys Thr Gly Thr Met Tyr Gly
      210          215          220
Val Ile Val Arg Ser Glu Gly Glu Asp Gly Lys Leu Phe Ile Gly Thr
      225          230          235          240
Ala Val Asp Gly Lys Gln Asp Tyr Phe Pro Thr Leu Ser Ser Arg Lys
          245          250          255
Leu Pro Arg Asp Pro Glu Ser Ser Ala Met Leu Asp Tyr Glu Leu His
          260          265          270
Ser Asp Phe Val Ser Ser Leu Ile Lys Ile Pro Ser Asp Thr Leu Ala
          275          280          285
Leu Val Ser His Phe Asp Ile Phe Tyr Ile Tyr Gly Phe Ala Ser Gly
      290          295          300
Gly Phe Val Tyr Phe Leu Thr Val Gln Pro Glu Thr Pro Glu Gly Val
      305          310          315          320
Ala Ile Asn Ser Ala Gly Asp Leu Phe Tyr Thr Ser Arg Ile Val Arg

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1..txt
325 330 335

Leu Cys Lys Asp Asp Pro Lys Phe His Ser Tyr Val Ser Leu Pro Phe
340 345 350
Gly Cys Thr Arg Ala Gly Val Glu Tyr Arg Leu Leu Gln Ala Ala Tyr
355 360 365
Leu Ala Lys Pro Gly Asp Ser Leu Ala Gln Ala Phe Asn Ile Thr Ser
370 375 380
Gln Asp Asp Val Leu Phe Ala Ile Phe Ser Lys Gly Gln Lys Gln Tyr
385 390 395 400
His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala
405 410 415
Ile Asn Leu Gln Ile Lys Glu Arg Leu Gln Ser Cys Tyr Gln Gly Glu
420 425 430
Gly Asn Leu Glu Leu Asn Trp Leu Leu Gly Lys Asp Val Gln Cys Thr
435 440 445
Lys Ala Pro Val Pro Ile Asp Asp Asn Phe Cys Gly Leu Asp Ile Asn
450 455 460
Gln Pro Leu Gly Gly Ser Thr Pro Val Glu Gly Leu Thr Leu Tyr Thr
465 470 475 480
Thr Ser Arg Asp Arg Met Thr Ser Val Ala Ser Tyr Val Tyr Asn Gly
485 490 495
Tyr Ser Val Val Phe Val Gly Thr Lys Ser Gly Lys Leu Lys Lys Val
500 505 510
Arg Val Tyr Glu Phe Arg Cys Ser Asn Ala Ile His Leu Leu Ser Lys
515 520 525
Glu Ser Leu Leu Glu Gly Ser Tyr Trp Trp Arg Phe Asn Tyr Arg Gln
530 535 540
Leu Tyr Phe Leu Gly Glu Gln Arg
545 550

<210> 171

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 171

tggaataaccg cctcctgcag

20

<210> 172

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 172
cttctgccct ttggagaaga tggc

24

<210> 173
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 173
ggactcactg gccaggcct tcaatatcac cagccaggac gat

43

<210> 174
<211> 3106
<212> DNA
<213> Homo sapiens

<220>
<221> modified_base
<222> (1683)..(1683)
<223> a, t, c or g

<400> 174
aggctcccgc ggcgaggctga gtgcggactg gagtgggaac ccgggtcccc gcgcttagag 60
aacacgcgat gaccacgtgg agcctccggc ggaggccggc ccgcacgctg ggactcctgc 120
tgctggctcgt cttgggcttc ctgggtgctcc gcaggctgga ctggagcacc ctggccctc 180
tgcggctccg ccatcgacag ctggggctgc aggccaaagg ctggaacttc atgctggagg 240
attccacctt ctggatcttc gggggctcca tccactatit ccgtgtgccc agggagtact 300
ggagggaccg cctgctgaag atgaaggcct gtggcttgaa caccctcacc acctatgttc 360
cgtggaacct gcatgagcca gaaagaggca aatttgactt ctctgggaac ctggacctgg 420
aggccttcgt cctgatggcc gcagagatcg ggctgtgggt gattctgctg ccaggccctc 480
acatctgcag tgagatggac ctcgggggct tgcccagctg gctactccaa gaccctggca 540
tgaggctgag gacaacttac aagggtcttc ccgaagcagt ggacctttat ttgaccacc 600
tgatgtccag ggtgggtgcca ctccagtaca agcgtggggg acctatcatt gccgtgcagg 660
tggagaatga atatggttcc tataataaag accccgcata catgccctac gtcaagaagg 720
cactggagga ccgtggcatt gtggaactgc tcctgacttc agacaacaag gatgggctga 780
gcaaggggat tgtccaggga gtcttggtcca ccatcaactt gcagtcaaca cagagctgc 840
agctactgac cacctttctc ttcaacgtcc aggggactca gcccaagatg gtgatggagt 900
actggacggg gtggtttgac tcgtggggag gccctcacia tatcttgat tcttctgagg 960
ttttgaaaac cgtgtctgcc attgtggacg ccggctcctc catcaacctc tacatgttcc 1020
acggaggcac caactttggc ttcatgaatg gagcatgca cttccatgac tacaagtacg 1080
atgtcaccag ctatgactat gatgctgtgc tgacagaagc cggcgattac acggccaagt 1140
acatgaagct tcgagacttc ttcggtcca tctcaggcat ccctctccct cccccacctg 1200
accttcttcc caagatgccg tatgagccct taacgccagt cttgtacctg tctctgtggg 1260
acgccctcaa gtacctgggg gagccaatca agtctgaaaa gcccatcaac atggagaacc 1320
tgccagtcac tgggggaaat ggacagtcct tcgggtacat tctctatgag accagcatca 1380
cctcgtctgg catcctcagt ggccacgtgc atgatcgggg gcaggtggtt gtgaacacag 1440
tatccatagg attcttggac tacaagacaa cgaagattgc tgtccccctg atccagggtt 1500
acaccgtgct gaggatcttg gtggagaatc gtgggagagt caactatggg gagaatattg 1560
atgaccagcg caaaggctta attggaaatc tctatctgaa tgattcacc ctgaaaaact 1620
tcagaatcta tagcctggat atgaagaaga gcttctttca gaggttcggc ctggacaaat 1680
ggngttccct cccagaaaca cccacattac ctgctttctt cttgggtagc ttgtccatca 1740
gtctccagcc ttgtgacacc tttctgaagc tggagggtcg ggagaagggg gttgtattca 1800
tcaatggcca gaaccttgga cgttactgga acattggacc ccagaagacg ctttacctcc 1860
cagggtccctg gttgagcagc ggaatcaacc aggtcatcgt ttttgaggag acgatggcgg 1920
gccctgcatt acagttcacg gaaaccccc acctgggcag gaaccagtac attaagtga 1980
cggtggcacc cctcctgct ggtgccagt ggagactgcc gcctcctctt gacctgaagc 2040

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ctggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg 2100
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaagggtg 2160
ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttggtgccg 2220
aggctgtcgg gctgtctcta ggggtgggagc agctaatacag atcgcccagc ctttgggccct 2280
cagaaaaagt gctgaaacgt gcccttgac cggacgtcac agccctgcga gcatctgctg 2340
gactcaggcg tgccttttg tggttcctgg gaggcttggc cacatccctc atggcccat 2400
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc 2460
tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa 2520
ctcggcgtga gaaacatgtg acttccccct tcccttccca ctcgctgctt cccacaggggt 2580
gacaggctgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcagggtgt 2640
ctctgggtgt cagtggaggag gacatgtgag tcctggcaga agccatggcc catgtctgca 2700
catccagggg ggaggacaga aggccagct cacatgtgag tcctggcaga agccatggcc 2760
catgtctgca catccaggga ggaggacaga aggccagct cacatgtgag tcctggcaga 2820
agccatggcc catgtctgca catccagggg ggaggacaga aggccagct cacatgtgag 2880
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gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac acctggcctg 3060
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<210> 175
 <211> 636
 <212> PRT
 <213> Homo sapiens

<220>
 <221> MOD_RES
 <222> (539)
 <223> Any amino acid

<400> 175
 Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
 1 5 10 15
 Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
 20 25 30
 Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
 35 40 45
 Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
 50 55 60
 Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
 65 70 75 80
 Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
 85 90 95
 Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
 100 105 110
 Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
 115 120 125
 Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
 130 135 140
 Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190

Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205

Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220

Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240

Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255

Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270

Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285

Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300

Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320

Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys
 325 330 335

Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly
 340 345 350

Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile
 355 360 365

Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro
 370 375 380

Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu
 385 390 395 400

Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu
 405 410 415

Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu
 420 425 430

Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His
 435 440 445

Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp
 450 455 460

Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val
 465 470 475 480

Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn
 485 490 495

Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp
 500 505 510

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser
515 520 525

Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Xaa Ser Leu Pro Glu Thr
530 535 540

Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr
545 550 555 560

Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
565 570 575

Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln
580 585 590

Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln
595 600 605

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr
610 615 620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys
625 630 635

<210> 176
<211> 2505
<212> DNA
<213> Homo sapiens

<400> 176
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ccctgggtgag ggttctctac ttggcccttcg gtgggggtca agacgcaggc acctacgcca 120
aaggggagca aagccgggct cggcccgagg cccccaggac ctccatctcc caatgttgga 180
ggaatccgac acgtgacggt ctgtccgccg tctcagacta gaggagcgct gtaaacgcca 240
tggtcccaa gaagctgtcc tgccttcgtt ccctgtgtgt gccgctcagc ctgacgctac 300
tgctgcccc ggcagacact cggtcggttc tagtgatag gggtcattgac cggtttctcc 360
tagacggggc cccgttccgc tatgtgtctg gcagcctgca ctactttcgg gtaccgcggg 420
tgctttgggc cgaccggctt ttgaagatgc gatggagcgg cctcaacgcc atacagtttt 480
atgtgccctg gaactaccac gagccacagc ctgggggtcta taactttaat ggcagccggg 540
acctcattgc ctttctgaat gaggcagctc tagcgaacct gttggtcata ctgagaccag 600
gaccttacat ctgtgcagag tgggagatgg ggggtctccc atcctgggtg cttcgaaaac 660
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ttcaggtgga gaatgaatat ggtagctaca gagcctgtga cttcagctac atgaggcact 840
tggtctgggt cttccgtgca ctgctaggag aaaagatctt gctcttcacc acagatgggc 900
ctgaaggact caagtgtggc tccctccggg gactctatac cactgtagat tttggcccag 960
ctgacaacat gacaaaaatc tttaccctgc ttcggaagta tgaaccccat gggccattgg 1020
taaactctga gtactacaca ggctgggtgg attactgggg ccagaatcac tccacacggg 1080
ctgtgtcagc tgtaacaaa ggactagaga acatgctcaa gttgggagcc agtgtgaaca 1140
tgtacatgtt ccatggaggt accaactttg gatattggaa tgggtccgat aagaaggagc 1200
gcttccttcc gattactacc agctatgact atgatgcacc tatacttgaa gcaggggacc 1260
ccacacctaa gctttttgct cttcgagatg tcatcagcaa gttccaggaa gttccttttg 1320
gacctttacc tcccccgagc cccaagatga tgcttgacc tgtgactctg cacttggttg 1380
ggcatttact ggttttctta gacttgcttt gccccgtgg gccattcat tcaatcttgc 1440
caatgacctt tgaggctgtc aagcaggacc atggcttcat gttgtaccga acctatatga 1500
cccataccat ttttgagcca acaccattct gggtgccaaa taatggagtc catgaccgtg 1560
cctatgtgat ggtggatggg gtgttccagg gtgttggtga gcgaaatatg agagacaaac 1620
tatttttgac ggggaaactg gggtcctaac tggatatctt ggtgggagaa atggggaggc 1680
tcagcttttg gtctaacagc agtgacttca agggcctgtt gaagccacca attctggggc 1740
aaacaattct taccagtggt atgatgttcc ctctgaaaat tgataacctt gtgaagtggg 1800
ggttttccct ccagttggca aaatggccat atcctcaagc tccttctggc cccacattct 1860
actccaaaac atttccaatt ttaggctcag ttggggacac atttctatat ctacctggat 1920
ggaccaaggg ccaagtctgg atcaatgggt ttaacttggg ccggtactgg acaaagcagg 1980

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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ggccacaaca gaccctctac gtgccaaagat tcctgctggt tcctagggga gccctcaaca 2040
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agcctatcct caatagcact agtactttgc acaggacaca tatcaattcc ctttcagctg 2160
atacactgag tgcctctgaa ccaatggagt taagtgggca ctgaaaggta ggccgggcat 2220
ggtggctcat gcctgtaatc ccagcacttt gggaggctga gacgggtgga ttacctgagg 2280
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aaattagccg ggcgtgatgg tgggcacctc taatcccagc tacttgggag gctgagggca 2400
ggagaattgc ttgaatccag gaggcagagg ttgcagtga tggaggtgt accactgcac 2460
tccagcctgg ctgacagtga gacactccat ctcaaaaaaa aaaaa 2505

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<210> 177
 <211> 654
 <212> PRT
 <213> Homo sapiens

<400> 177

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Met Ala Pro Lys Lys Leu Ser Cys Leu Arg Ser Leu Leu Leu Pro Leu
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Ser Leu Thr Leu Leu Leu Pro Gln Ala Asp Thr Arg Ser Phe Val Val
          20           25          30
Asp Arg Gly His Asp Arg Phe Leu Leu Asp Gly Ala Pro Phe Arg Tyr
      35           40          45
Val Ser Gly Ser Leu His Tyr Phe Arg Val Pro Arg Val Leu Trp Ala
      50           55          60
Asp Arg Leu Leu Lys Met Arg Trp Ser Gly Leu Asn Ala Ile Gln Phe
      65           70          75          80
Tyr Val Pro Trp Asn Tyr His Glu Pro Gln Pro Gly Val Tyr Asn Phe
          85           90          95
Asn Gly Ser Arg Asp Leu Ile Ala Phe Leu Asn Glu Ala Ala Leu Ala
      100          105          110
Asn Leu Leu Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ala Glu Trp
      115          120          125
Glu Met Gly Gly Leu Pro Ser Trp Leu Leu Arg Lys Pro Glu Ile His
      130          135          140
Leu Arg Thr Ser Asp Pro Asp Phe Leu Ala Ala Val Asp Ser Trp Phe
      145          150          155          160
Lys Val Leu Leu Pro Lys Ile Tyr Pro Trp Leu Tyr His Asn Gly Gly
      165          170          175
Asn Ile Ile Ser Ile Gln Val Glu Asn Glu Tyr Gly Ser Tyr Arg Ala
      180          185          190
Cys Asp Phe Ser Tyr Met Arg His Leu Ala Gly Leu Phe Arg Ala Leu
      195          200          205
Leu Gly Glu Lys Ile Leu Leu Phe Thr Thr Asp Gly Pro Glu Gly Leu
      210          215          220
Lys Cys Gly Ser Leu Arg Gly Leu Tyr Thr Thr Val Asp Phe Gly Pro
      225          230          235          240
Ala Asp Asn Met Thr Lys Ile Phe Thr Leu Leu Arg Lys Tyr Glu Pro
      245          250          255

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Gly Pro Leu Val Asn Ser Glu Tyr Tyr Thr Gly Trp Leu Asp Tyr
260 265 270

Trp Gly Gln Asn His Ser Thr Arg Ser Val Ser Ala Val Thr Lys Gly
275 280 285

Leu Glu Asn Met Leu Lys Leu Gly Ala Ser Val Asn Met Tyr Met Phe
290 295 300

His Gly Gly Thr Asn Phe Gly Tyr Trp Asn Gly Ala Asp Lys Lys Gly
305 310 315 320

Arg Phe Leu Pro Ile Thr Thr Ser Tyr Asp Tyr Asp Ala Pro Ile Ser
325 330 335

Glu Ala Gly Asp Pro Thr Pro Lys Leu Phe Ala Leu Arg Asp Val Ile
340 345 350

Ser Lys Phe Gln Glu Val Pro Leu Gly Pro Leu Pro Pro Ser Pro
355 360 365

Lys Met Met Leu Gly Pro Val Thr Leu His Leu Val Gly His Leu Leu
370 375 380

Ala Phe Leu Asp Leu Leu Cys Pro Arg Gly Pro Ile His Ser Ile Leu
385 390 395 400

Pro Met Thr Phe Glu Ala Val Lys Gln Asp His Gly Phe Met Leu Tyr
405 410 415

Arg Thr Tyr Met Thr His Thr Ile Phe Glu Pro Thr Pro Phe Trp Val
420 425 430

Pro Asn Asn Gly Val His Asp Arg Ala Tyr Val Met Val Asp Gly Val
435 440 445

Phe Gln Gly Val Val Glu Arg Asn Met Arg Asp Lys Leu Phe Leu Thr
450 455 460

Gly Lys Leu Gly Ser Lys Leu Asp Ile Leu Val Glu Asn Met Gly Arg
465 470 475 480

Leu Ser Phe Gly Ser Asn Ser Ser Asp Phe Lys Gly Leu Leu Lys Pro
485 490 495

Pro Ile Leu Gly Gln Thr Ile Leu Thr Gln Trp Met Met Phe Pro Leu
500 505 510

Lys Ile Asp Asn Leu Val Lys Trp Trp Phe Pro Leu Gln Leu Pro Lys
515 520 525

Trp Pro Tyr Pro Gln Ala Pro Ser Gly Pro Thr Phe Tyr Ser Lys Thr
530 535 540

Phe Pro Ile Leu Gly Ser Val Gly Asp Thr Phe Leu Tyr Leu Pro Gly
545 550 555 560

Trp Thr Lys Gly Gln Val Trp Ile Asn Gly Phe Asn Leu Gly Arg Tyr
565 570 575

Trp Thr Lys Gln Gly Pro Gln Gln Thr Leu Tyr Val Pro Arg Phe Leu
580 585 590

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Phe Pro Arg Gly Ala Leu Asn Lys Ile Thr Leu Leu Glu Leu Glu
595 600 605

Asp Val Pro Leu Gln Pro Gln Val Gln Phe Leu Asp Lys Pro Ile Leu
610 615 620

Asn Ser Thr Ser Thr Leu His Arg Thr His Ile Asn Ser Leu Ser Ala
625 630 635 640

Asp Thr Leu Ser Ala Ser Glu Pro Met Glu Leu Ser Gly His
645 650

<210> 178

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 178

tggctactcc aagaccctgg catg

24

<210> 179

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 179

tggacaaatc cccttgctca gccc

24

<210> 180

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 180

gggcttcacc gaagcagtgg acctttatatt tgaccacctg atgtccaggg

50

<210> 181

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 181

ccagctatga ctatgatgca cc

22

<210> 182

<211> 24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 182

tggcaccag aatggtgttg gctc

24

<210> 183

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 183

cgagatgtca tcagcaagtt ccaggaagtt cctttgggac ctttacctcc

50

<210> 184

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 184

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gtgtttatgg ctttatctgc ctctacactc tcttctgggt attcaggata ctttgaagg 180
aatattcttt cgaaaaagtc agagaagaga gcagttttag tgacattcca gatgtcaaaa 240
acgattttgc gttccttctt cacatggtag accagtatga ccagctatat tccaagcgtt 300
ttggtgtggt cttgtcagaa gttagtgaaa ataaacttag ggaaattagt ttgaaccatg 360
agtggacatt tgaaaaactc aggcagcaca ttacacgcaa cgcccaggac aagcaggagt 420
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aggggaaggaa aaattataat cactaatctt gggtcttttt aaattgtttg taacttggat 1860
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ttttcttact aaaaaaaaaa aaaaaaa 1947

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<210> 185

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 501

<212> PRT

<213> Homo sapiens

<400> 185

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          20          25          30
Ile Pro Leu Lys Glu Tyr Ser Phe Glu Lys Val Arg Glu Glu Ser Ser
          35          40          45
Phe Ser Asp Ile Pro Asp Val Lys Asn Asp Phe Ala Phe Leu Leu His
          50          55          60
Met Val Asp Gln Tyr Asp Gln Leu Tyr Ser Lys Arg Phe Gly Val Phe
          65          70          75          80
Leu Ser Glu Val Ser Glu Asn Lys Leu Arg Glu Ile Ser Leu Asn His
          85          90          95
Glu Trp Thr Phe Glu Lys Leu Arg Gln His Ile Ser Arg Asn Ala Gln
          100          105          110
Asp Lys Gln Glu Leu His Leu Phe Met Leu Ser Gly Val Pro Asp Ala
          115          120          125
Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro
          130          135          140
Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu
          145          150          155          160
Leu His Leu Cys His Cys Pro Ala Lys Val Glu Gln Thr Ala Phe Ser
          165          170          175
Phe Leu Arg Asp His Leu Arg Cys Leu His Val Lys Phe Thr Asp Val
          180          185          190
Ala Glu Ile Pro Ala Trp Val Tyr Leu Leu Lys Asn Leu Arg Glu Leu
          195          200          205
Tyr Leu Ile Gly Asn Leu Asn Ser Glu Asn Asn Lys Met Ile Gly Leu
          210          215          220
Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser
          225          230          235          240
Asn Leu Thr Lys Val Pro Ser Asn Ile Thr Asp Val Ala Pro His Leu
          245          250          255
Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn
          260          265          270
Ser Leu Lys Lys Met Met Asn Val Ala Glu Leu Glu Leu Gln Asn Cys
          275          280          285
Glu Leu Glu Arg Ile Pro His Ala Ile Phe Ser Leu Ser Asn Leu Gln
          290          295          300
Glu Leu Asp Leu Lys Ser Asn Asn Ile Arg Thr Ile Glu Glu Ile Ile

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

305 310 315 320
 Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn
 325 330 335
 Lys Ile Val Thr Ile Pro Pro Ser Ile Thr His Val Lys Asn Leu Glu
 340 345 350
 Ser Leu Tyr Phe Ser Asn Asn Lys Leu Glu Ser Leu Pro Val Ala Val
 355 360 365
 Phe Ser Leu Gln Lys Leu Arg Cys Leu Asp Val Ser Tyr Asn Asn Ile
 370 375 380
 Ser Met Ile Pro Ile Glu Ile Gly Leu Leu Gln Asn Leu Gln His Leu
 385 390 395 400
 His Ile Thr Gly Asn Lys Val Asp Ile Leu Pro Lys Gln Leu Phe Lys
 405 410 415
 Cys Ile Lys Leu Arg Thr Leu Asn Leu Gly Gln Asn Cys Ile Thr Ser
 420 425 430
 Leu Pro Glu Lys Val Gly Gln Leu Ser Gln Leu Thr Gln Leu Glu Leu
 435 440 445
 Lys Gly Asn Cys Leu Asp Arg Leu Pro Ala Gln Leu Gly Gln Cys Arg
 450 455 460
 Met Leu Lys Lys Ser Gly Leu Val Val Glu Asp His Leu Phe Asp Thr
 465 470 475 480
 Leu Pro Leu Glu Val Lys Glu Ala Leu Asn Gln Asp Ile Asn Ile Pro
 485 490 495
 Phe Ala Asn Gly Ile
 500

<210> 186
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 186
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<210> 187
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 187
 gaccaacttt ctctgggagt gagg 24

<210> 188

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 188

gtcactttat ttctctaaca acaagctcga atccttacca gtggcag

47

<210> 189

<211> 2917

<212> DNA

<213> Homo sapiens

<400> 189

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aagacatttg tgttttacac acataaggat ctgtgttttg ggtttcttct tcctcccctg 180
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tcttgtcctg ccctgcagtg ctgtgaagga tatagaatgt gtgccagttt tgattccctg 540
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gaaactccaa accagccttt caacagtgtg catctgtttt ccttcatggg tctagctctg 2700
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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 ggcctgaaag tgacacacag gcctgcatgt aaaaaaa 2917

<210> 190
 <211> 607
 <212> PRT
 <213> Homo sapiens

<400> 190
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 20 25 30
 Thr Val Ser Leu Gly Gly Ala Asn Met Ala Glu Thr His Lys Ala Met
 35 40 45
 Ile Leu Gln Leu Asn Pro Ser Glu Asn Cys Thr Trp Thr Ile Glu Arg
 50 55 60
 Pro Glu Asn Lys Ser Ile Arg Ile Ile Phe Ser Tyr Val Gln Leu Asp
 65 70 75 80
 Pro Asp Gly Ser Cys Glu Ser Glu Asn Ile Lys Val Phe Asp Gly Thr
 85 90 95
 Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr
 100 105 110
 Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val
 115 120 125
 Thr Asp Ser Ala Arg Ile Gln Arg Thr Val Phe Val Phe Tyr Tyr Phe
 130 135 140
 Phe Ser Pro Asn Ile Ser Ile Pro Asn Cys Gly Gly Tyr Leu Asp Thr
 145 150 155 160
 Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu
 165 170 175
 Leu Ala Tyr Cys Val Trp His Ile Gln Val Glu Lys Asp Tyr Lys Ile
 180 185 190
 Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys
 195 200 205
 Phe Asp Phe Leu Ala Ile Tyr Asp Gly Pro Ser Thr Asn Ser Gly Leu
 210 215 220
 Ile Gly Gln Val Cys Gly Arg Val Thr Pro Thr Phe Glu Ser Ser Ser
 225 230 235 240
 Asn Ser Leu Thr Val Val Leu Ser Thr Asp Tyr Ala Asn Ser Tyr Arg
 245 250 255
 Gly Phe Ser Ala Ser Tyr Thr Ser Ile Tyr Ala Glu Asn Ile Asn Thr
 260 265 270
 Thr Ser Leu Thr Cys Ser Ser Asp Arg Met Arg Val Ile Ile Ser Lys
 275 280 285

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Tyr Leu Glu Ala Phe Asn Ser Asn Gly Asn Asn Leu Gln Leu Lys
290 295 300

Asp Pro Thr Cys Arg Pro Lys Leu Ser Asn Val Val Glu Phe Ser Val
305 310 315 320

Pro Leu Asn Gly Cys Gly Thr Ile Arg Lys Val Glu Asp Gln Ser Ile
325 330 335

Thr Tyr Thr Asn Ile Ile Thr Phe Ser Ala Ser Ser Thr Ser Glu Val
340 345 350

Ile Thr Arg Gln Lys Gln Leu Gln Ile Ile Val Lys Cys Glu Met Gly
355 360 365

His Asn Ser Thr Val Glu Ile Ile Tyr Ile Thr Glu Asp Asp Val Ile
370 375 380

Gln Ser Gln Asn Ala Leu Gly Lys Tyr Asn Thr Ser Met Ala Leu Phe
385 390 395 400

Glu Ser Asn Ser Phe Glu Lys Thr Ile Leu Glu Ser Pro Tyr Tyr Val
405 410 415

Asp Leu Asn Gln Thr Leu Phe Val Gln Val Ser Leu His Thr Ser Asp
420 425 430

Pro Asn Leu Val Val Phe Leu Asp Thr Cys Arg Ala Ser Pro Thr Ser
435 440 445

Asp Phe Ala Ser Pro Thr Tyr Asp Leu Ile Lys Ser Gly Cys Ser Arg
450 455 460

Asp Glu Thr Cys Lys Val Tyr Pro Leu Phe Gly His Tyr Gly Arg Phe
465 470 475 480

Gln Phe Asn Ala Phe Lys Phe Leu Arg Ser Met Ser Ser Val Tyr Leu
485 490 495

Gln Cys Lys Val Leu Ile Cys Asp Ser Ser Asp His Gln Ser Arg Cys
500 505 510

Asn Gln Gly Cys Val Ser Arg Ser Lys Arg Asp Ile Ser Ser Tyr Lys
515 520 525

Trp Lys Thr Asp Ser Ile Ile Gly Pro Ile Arg Leu Lys Arg Asp Arg
530 535 540

Ser Ala Ser Gly Asn Ser Gly Phe Gln His Glu Thr His Ala Glu Glu
545 550 555 560

Thr Pro Asn Gln Pro Phe Asn Ser Val His Leu Phe Ser Phe Met Val
565 570 575

Leu Ala Leu Asn Val Val Thr Val Ala Thr Ile Thr Val Arg His Phe
580 585 590

Val Asn Gln Arg Ala Asp Tyr Lys Tyr Gln Lys Leu Gln Asn Tyr
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<210> 191

<211> 21

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 191

tctctattcc aaactgtggc g

21

<210> 192

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 192

tttggatgacg attcgaaggt gg

22

<210> 193

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 193

ggaaggatcc ttcaccagcc ccaattaccc aaagccgcat cctgagc

47

<210> 194

<211> 2362

<212> DNA

<213> Homo sapiens

<400> 194

| | | | | | | |
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| cgggacatgc | ggccccagga | gctccccagg | ctcgcgttcc | cgttgctgct | gttgctgttg | 120 |
| ctgctgctgc | cgccgcgccc | gtgccctgcc | cacagcgcca | cgcgcttcga | ccccacctgg | 180 |
| gagtccttgg | acgcccgcga | gctgcccgcg | tggtttgacc | aggccaagtt | cggcatcttc | 240 |
| atccactggg | gagtggtttc | cgtgcccagc | ttcggtagcg | agtgggttctg | gtgggtattgg | 300 |
| caaaaggaaa | agataccgaa | gtatgtggaa | tttatgaaag | ataattaccc | tcctagtttc | 360 |
| aaatatgaag | attttgagcc | actatttaca | gcaaaatttt | ttaatgccaa | ccagtgggca | 420 |
| gatatttttc | aggcctctgg | tgccaaatac | attgtcttaa | cttccaaaca | tcatgaaggc | 480 |
| tttaccttgt | gggggtcaga | atattcgtgg | aactggaatg | ccatagatga | ggggcccaag | 540 |
| agggacattg | tcaaggaact | tgaggtagcc | attaggaaca | gaactgacct | gcgttttgga | 600 |
| ctgtactatt | ccctttttga | atgggtttcat | ccgctcttcc | ttgaggatga | atccagtcca | 660 |
| ttccataagc | ggcaatttcc | agtttctaag | acattgccag | agctctatga | gttagtgaac | 720 |
| aactatcagc | ctgaggttct | gtggtcggat | ggtgacggag | gagcaccgga | tcaatactgg | 780 |
| aacagcacag | gcttcttggc | ctgggttatat | aatgaaagcc | cagttcgggg | cacagtagtc | 840 |
| accaatgata | ggtggggagc | tggtagcatc | tgtaagcatg | gtggcttcta | tacctgcagt | 900 |
| gatcggtata | acccaggaca | tcttttgcca | cataaatggg | aaaactgcat | gacaatagac | 960 |
| aaactgtcct | ggggctatag | gagggaagct | ggaatctctg | actatcttac | aattgaagaa | 1020 |
| ttggtgaagc | aacttgttaga | gacagtttca | tgtggaggaa | atcttttgat | gaatattggg | 1080 |
| cccacactag | atggcaccat | ttctgtagtt | tttgaggagc | gactgaggca | agtgggggtcc | 1140 |
| tggtctaaaag | tcaatggaga | agctatttat | gaaacctata | cctggcgatc | ccagaatgac | 1200 |
| actgtcacc | cagatgtgtg | gtacacatcc | aagcctaaag | aaaaattagt | ctatgccatt | 1260 |
| tttcttaaat | ggccacatc | aggacagctg | ttccttggcc | atcccaaagc | tattctgggg | 1320 |
| gcaacagagg | tgaaactact | gggccatgga | cagccactta | actggatttc | tttggagcaa | 1380 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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taaactcatt gtgcaaatgt aa 2362

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<210> 195
 <211> 467
 <212> PRT
 <213> Homo sapiens

<400> 195

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          20          25          30
Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
          35          40          45
Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe
          50          55          60
Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys
          65          70          75          80
Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro
          85          90          95
Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe
          100          105          110
Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr
          115          120          125
Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser
          130          135          140
Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp
          145          150          155          160
Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg
          165          170          175
Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu
          180          185          190
Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys
          195          200          205

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val
210 215 220

Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser
225 230 235 240

Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr
245 250 255

Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly
260 265 270

Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro
275 280 285

His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr
290 295 300

Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val
305 310 315 320

Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn
325 330 335

Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
340 345 350

Leu Arg Gln Val Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
355 360 365

Glu Thr Tyr Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
370 375 380

Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
385 390 395 400

Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
405 410 415

Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
420 425 430

Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
435 440 445

Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
450 455 460

Asn Val Ile
465

<210> 196

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 196

tggtttgacc aggccaagtt cgg

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 197

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 197

ggattcatcc tcaaggaaga gcgg

24

<210> 198

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 198

aacttgagc atcagccact ctgc

24

<210> 199

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 199

ttccgtgccc agcttcggtg gcgagtggtt ctggtggtat tggca

45

<210> 200

<211> 2372

<212> DNA

<213> Homo sapiens

<400> 200

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agcaggggaaa tccggatgtc tcggttatga agtggagcag tgagtgtgag cctcaacata 60
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catctgaggt gtttcccttg ctctgaaggg gtaggcacga tggccagggt cttcagcctg 180
gtgttgcttc tcaacttccat ctggaccacg aggtccttgg tccaaggctc tttgcgtgca 240
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tgaggagaca cacctgaggt tggtttcttt catgctcctt accctgcccc agctggggaa 1200
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gtcctaataa tatcccactg ggagaaagga gttttgcaaa gtgcaaggac ctaaaacatc 1440
tcatcagtat ccagtggtaa aaaggcctcc tggctgtctg aggctagggtg ggttgaaagc 1500
caaggagtca ctgagaccacaa ggctttctct actgattccg cagctcagac cctttcttca 1560
gctctgaaag agaaacacgt atcccacctg acatgtcctt ctgagcccgg taagagcaaa 1620
agaatggcag aaaagttag cccctgaaag ccatggagat tctcataact tgagacctaa 1680
tctctgtaaa gctaaaataa agaaatagaa caaggctgag gatacgacag tacactgtca 1740
gcagggactg taaacacaga caggggtcaaa gtgttttctc tgaacacatt gagttggaat 1800
cactgtttag aacacacaga cttacttttt ctggtctcta ccactgctga tattttctct 1860
aggaaatata cttttacaag taacaaaaat aaaaactctt ataaatttct atttttatct 1920
gagttacaga aatgattact aaggaagatt actcagtaat ttgtttaaaa agtaataaaa 1980
ttcaacaaac atttgctgaa tagctactat atgtcaagtg ctgtgcaagg tattacactc 2040
tgtaattgaa tattattcct caaaaaattg cacatagtag aacgctatct gggaagctat 2100
ttttttcagt tttgatattt ctagcttatt tacttccaaa ctaattttta tttttgctga 2160
gactaatctt attcattttc tctaatatgg caaccattat aaccttaatt tattattaac 2220
atacctaaga agtacattgt tacctctata taccaaagca cattttaaaa gtgccattaa 2280
caaatgtatc actagccctc ctttttccaa caagaaggga ctgagagatg cagaaatatt 2340
tgtgacaaaa aattaaagca tttagaaaac tt 2372

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<210> 201

<211> 322

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic protein

<400> 201

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1 5 10 15

Thr Arg Leu Leu Val Gln Gly Ser Leu Arg Ala Glu Glu Leu Ser Ile
20 25 30

Gln Val Ser Cys Arg Ile Met Gly Ile Thr Leu Val Ser Lys Lys Ala
35 40 45

Asn Gln Gln Leu Asn Phe Thr Glu Ala Lys Glu Ala Cys Arg Leu Leu
50 55 60

Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala
65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val
85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly
100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys
115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile
130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr
145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser
165 170 175

Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu
195 200 205
Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala
210 215 220
Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu
225 230 235 240
Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe
245 250 255
Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn
260 265 270
Gln Gln Lys Glu Met Ile Glu Thr Lys Val Val Lys Glu Glu Lys Ala
275 280 285
Asn Asp Ser Asn Pro Asn Glu Glu Ser Lys Lys Thr Asp Lys Asn Pro
290 295 300
Glu Glu Ser Lys Ser Pro Ser Lys Thr Thr Val Arg Cys Leu Glu Ala
305 310 315 320
Glu Val

<210> 202
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 202
gagctttcca tccaggtgtc atgc

24

<210> 203
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 203
gtcagtgaca gtacctactc gg

22

<210> 204
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 204

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
 24

<210> 205
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 205
 aggagcctg taggctgctg ggactaagtt tggccggcaa ggaccaagtt 50

<210> 206
 <211> 1620
 <212> DNA
 <213> Homo sapiens

<220>
 <221> modified_base
 <222> (973)..(973)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (977)..(977)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (996)..(996)
 <223> a, t, c or g

<220>
 <221> modified_base
 <222> (1003)..(1003)
 <223> a, t, c or g

<400> 206
 agatggcggt cttggcacct ctaattgctc tcgtgtattc ggtgccgcga ctttcacgat 60
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 ggaaactgcc gccgctctgc cacggtctgc ccaccaacg cgaagacggt aaccctgtgt 180
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 accgcagatc catcactgtg gagcaacata taggcaacat tttcatgttt agtaaagtgg 300
 ccaacacaat tcttttcttc cgcttgata ttcgcatggg cctactttac atcacactct 360
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 acttcaatga taaaaccatt gatgaggaac tagaacggga caagagggtc acttggattg 480
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 tctcccttaa atacaactgt acaggggctaa attttgggaa ggtggatgtt ggacgctata 600
 ctgatgttag tacgcggtac aaagttagca catcaccctt caccaagcaa ctccctaccc 660
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 gggctgtctc atggaccttc tctgaggaga atgtgatccg agaatttaac ttaaatgagc 780
 tataccagcg ggccaagaaa ctatcaaagg ctggagacaa tatccctgag gaggcagcctg 840
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 gctgcagcct ttnattnatg ttttcccttt ggctgngact ggntggggca gcatgcagct 1020
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 tttctccatg aaactctgtg gtttcatcat tccttcttag ttgacctgca cagcttggtt 1260
 agacctagat ttaaccctaa ggtaagatgc tggggatatag aacgctaaga attttcccc 1320
 aaggactctt gcttccttaa gcccttctgg cttcgtttat ggtcttcatt aaaagtataa 1380

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

gcctaacttt gtcgctagtc ctaaggagaa acctttaacc acaaagtttt tatcattgaa 1440
gacaatattg aacaaccccc tattttgtgg ggattgagaa ggggtgaata gaggcttgag 1500
actttccttt gtgtggtagg acttggagga gaaatcccct ggactttcac taaccctctg 1560
acatactccc cacaccagtg tgatggcttt ccgtaataaa aagattggga tttccttttg 1620

<210> 207
<211> 296
<212> PRT
<213> Homo sapiens

<400> 207
Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
1 5 10 15
Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
20 25 30
Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
35 40 45
Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
50 55 60
Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
65 70 75 80
Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe
85 90 95
Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met
100 105 110
Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys
115 120 125
Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys
130 135 140
Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val
145 150 155 160
Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile
165 170 175
Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
180 185 190
Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val
195 200 205
Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln
210 215 220
Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg
225 230 235 240
Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe Asn
245 250 255
Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp
260 265 270
Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val Ser

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Asp Gly Glu Asn Lys Lys Asp Lys
290 295

<210> 208

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 208

gcttgatata tcgcatgggc ctac

24

<210> 209

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 209

tgagacaat atccctgagg

20

<210> 210

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 210

aacagttggc cacagcatgg cagg

24

<210> 211

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 211

ccattgatga ggaactagaa cgggacaaga gggtcacttg gattgtggag

50

<210> 212

<211> 1985

<212> DNA

<213> Homo sapiens

<400> 212

ggacagctcg cggccccga gagctctagc cgtcaggag ctgcctgggg acgtttgccc 60
tggggccccca gcctggccc ggtcaccctg gcatgaggag atgggcctgt tgctcctggg 120
cccattgctc ctgctgccc gctcctacgg actgcccttc tacaacggct tctactactc 180
caacagcgcc aacgaccaga acctaggcaa cggtcattgg aaagacctcc ttaatggagt 240

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gaagctggtg gtggagacac ccgaggagac cctgttcacc taccaagggg ccagtgtgat 300
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaa

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<210> 213
 <211> 360
 <212> PRT
 <213> Homo sapiens

<400> 213
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 1 5 10 15
 Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser Asn Ser Ala Asn Asp
 20 25 30
 Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu Leu Asn Gly Val Lys
 35 40 45
 Leu Val Val Glu Thr Pro Glu Glu Thr Leu Phe Thr Tyr Gln Gly Ala
 50 55 60
 Ser Val Ile Leu Pro Cys Arg Tyr Arg Tyr Glu Pro Ala Leu Val Ser
 65 70 75 80
 Pro Arg Arg Val Arg Val Lys Trp Trp Lys Leu Ser Glu Asn Gly Ala
 85 90 95
 Pro Glu Lys Asp Val Leu Val Ala Ile Gly Leu Arg His Arg Ser Phe
 100 105 110
 Gly Asp Tyr Gln Gly Arg Val His Leu Arg Gln Asp Lys Glu His Asp
 115 120 125
 Val Ser Leu Glu Ile Gln Asp Leu Arg Leu Glu Asp Tyr Gly Arg Tyr
 130 135 140

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Cys Glu Val Ile Asp Gly Leu Glu Asp Glu Ser Gly Leu Val Glu
145 150 155 160
Leu Glu Leu Arg Gly Val Val Phe Pro Tyr Gln Ser Pro Asn Gly Arg
165 170 175
Tyr Gln Phe Asn Phe His Glu Gly Gln Gln Val Cys Ala Glu Gln Ala
180 185 190
Ala Val Val Ala Ser Phe Glu Gln Leu Phe Arg Ala Trp Glu Glu Gly
195 200 205
Leu Asp Trp Cys Asn Ala Gly Trp Leu Gln Asp Ala Thr Val Gln Tyr
210 215 220
Pro Ile Met Leu Pro Arg Gln Pro Cys Gly Gly Pro Gly Leu Ala Pro
225 230 235 240
Gly Val Arg Ser Tyr Gly Pro Arg His Arg Arg Leu His Arg Tyr Asp
245 250 255
Val Phe Cys Phe Ala Thr Ala Leu Lys Gly Arg Val Tyr Tyr Leu Glu
260 265 270
His Pro Glu Lys Leu Thr Leu Thr Glu Ala Arg Glu Ala Cys Gln Glu
275 280 285
Asp Asp Ala Thr Ile Ala Lys Val Gly Gln Leu Phe Ala Ala Trp Lys
290 295 300
Phe His Gly Leu Asp Arg Cys Asp Ala Gly Trp Leu Ala Asp Gly Ser
305 310 315 320
Val Arg Tyr Pro Val Val His Pro His Pro Asn Cys Gly Pro Pro Glu
325 330 335
Pro Gly Val Arg Ser Phe Gly Phe Pro Asp Pro Gln Ser Arg Leu Tyr
340 345 350
Gly Val Tyr Cys Tyr Arg Gln His
355 360

<210> 214

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 214

tgcttcgcta ctgccctc

18

<210> 215

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 215
ttcccttggtg ggttgag 18

<210> 216
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 216
agggtggaa gccagttc 18

<210> 217
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 217
agccagtgg gaaatgag 18

<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 218
tgtccaaagt acacacacct gagg 24

<210> 219
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 219
gatgccacga tcgccaaggt gggacagctc tttgccgcct ggaag 45

<210> 220
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 220
ggagagcggg gccaagctgg ataacagggg accgatgatg tggcgaccat cagttctgct 60
gcttctgttg ctactgaggc acggggccca ggggaagcca tccccagacg caggccctca 120
tggccagggg aggggtgcacc aggcggcccc cctgagcgac gctccccatg atgacgcca 180
cggaacttc cagtacgacc atgaggcttt cctgggacgg gaagtggcca aggaattcga 240
ccaactcacc ccagaggaaa gccaggcccc tctggggcgg atcgtggacc gcatggaccg 300

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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cgcggggggac ggcgacggct ggggtgtcgt ggccgagctt cgcgcgtgga tcgcgcacac 360
gcagcagcgg cacatacggg actcgggtgag cgccggcctgg gacacgtacg acacggaccg 420
cgacgggctgt gtgggtttggg aggagctgct caacgccacc tatggccact acgcgcccgg 480
tgaagaattt catgacgtgg aggatgcaga gacctacaaa aagatgctgg ctcgggacga 540
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<210> 221
 <211> 328
 <212> PRT
 <213> Homo sapiens

<400> 221
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 Arg Val His Gln Ala Ala Pro Leu Ser Asp Ala Pro His Asp Asp Ala
 35 40 45
 His Gly Asn Phe Gln Tyr Asp His Glu Ala Phe Leu Gly Arg Glu Val
 50 55 60
 Ala Lys Glu Phe Asp Gln Leu Thr Pro Glu Glu Ser Gln Ala Arg Leu
 65 70 75 80
 Gly Arg Ile Val Asp Arg Met Asp Arg Ala Gly Asp Gly Asp Gly Trp
 85 90 95
 Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg
 100 105 110
 His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp
 115 120 125
 Arg Asp Gly Arg Val Gly Trp Glu Glu Leu Arg Asn Ala Thr Tyr Gly
 130 135 140
 His Tyr Ala Pro Gly Glu Glu Phe His Asp Val Glu Asp Ala Glu Thr
 145 150 155 160
 Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp
 165 170 175
 Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu
 180 185 190

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr
195 200 205
Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu
210 215 220
Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala
225 230 235 240
Trp Val Gln Thr Glu Arg Gln Gln Phe Arg Asp Phe Arg Asp Leu Asn
245 250 255
Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro
260 265 270
Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu
275 280 285
Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly
290 295 300
Asn Trp Asn Met Phe Val Gly Ser Gln Ala Thr Asn Tyr Gly Glu Asp
305 310 315 320
Leu Thr Arg His His Asp Glu Leu
325

<210> 222

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 222

cgcaggccct catggccagg

20

<210> 223

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 223

gaaatcctgg gtaattgg

18

<210> 224

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 224

gtgcgcggtg ctcacagctc atc

23

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 225

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide probe

<400> 225

ccccctgag cgacgctccc ccatgatgac gccacggga actt

44

<210> 226

<211> 2403

<212> DNA

<213> Homo sapiens

<400> 226

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atcctgggct tcgctcgatt tgccgcccag gcgcctccca gacctagagg ggcgctggcc 240
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gattagaacc aattgtttct gatgtcatca gaggcatttg tagagatttc ttagaatccc 2040
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<210> 227

<211> 550

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> PRT

<213> Homo sapiens

<400> 227

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Leu Leu Pro Gly Pro Ala Gly Ser Glu Gly Ala Ala Pro Ile Ala Ile
      20      25      30
Thr Cys Phe Thr Arg Gly Leu Asp Ile Arg Lys Glu Lys Ala Asp Val
      35      40      45
Leu Cys Pro Gly Gly Cys Pro Leu Glu Glu Phe Ser Val Tyr Gly Asn
      50      55      60
Ile Val Tyr Ala Ser Val Ser Ser Ile Cys Gly Ala Ala Val His Arg
      65      70      75      80
Gly Val Ile Ser Asn Ser Gly Gly Pro Val Arg Val Tyr Ser Leu Pro
      85      90      95
Gly Arg Glu Asn Tyr Ser Ser Val Asp Ala Asn Gly Ile Gln Ser Gln
      100     105     110
Met Leu Ser Arg Trp Ser Ala Ser Phe Thr Val Thr Lys Gly Lys Ser
      115     120     125
Ser Thr Gln Glu Ala Thr Gly Gln Ala Val Ser Thr Ala His Pro Pro
      130     135     140
Thr Gly Lys Arg Leu Lys Lys Thr Pro Glu Lys Lys Thr Gly Asn Lys
      145     150     155     160
Asp Cys Lys Ala Asp Ile Ala Phe Leu Ile Asp Gly Ser Phe Asn Ile
      165     170     175
Gly Gln Arg Arg Phe Asn Leu Gln Lys Asn Phe Val Gly Lys Val Ala
      180     185     190
Leu Met Leu Gly Ile Gly Thr Glu Gly Pro His Val Gly Leu Val Gln
      195     200     205
Ala Ser Glu His Pro Lys Ile Glu Phe Tyr Leu Lys Asn Phe Thr Ser
      210     215     220
Ala Lys Asp Val Leu Phe Ala Ile Lys Glu Val Gly Phe Arg Gly Gly
      225     230     235     240
Asn Ser Asn Thr Gly Lys Ala Leu Lys His Thr Ala Gln Lys Phe Phe
      245     250     255
Thr Val Asp Ala Gly Val Arg Lys Gly Ile Pro Lys Val Val Val Val
      260     265     270
Phe Ile Asp Gly Trp Pro Ser Asp Asp Ile Glu Glu Ala Gly Ile Val
      275     280     285
Ala Arg Glu Phe Gly Val Asn Val Phe Ile Val Ser Val Ala Lys Pro
      290     295     300
Ile Pro Glu Glu Leu Gly Met Val Gln Asp Val Thr Phe Val Asp Lys
      305     310     315     320

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Val Cys Arg Asn Asn Gly Phe Phe Ser Tyr His Met Pro Asn Trp
325 330 335

Phe Gly Thr Thr Lys Tyr Val Lys Pro Leu Val Gln Lys Leu Cys Thr
340 345 350

His Glu Gln Met Met Cys Ser Lys Thr Cys Tyr Asn Ser Val Asn Ile
355 360 365

Ala Phe Leu Ile Asp Gly Ser Ser Ser Val Gly Asp Ser Asn Phe Arg
370 375 380

Leu Met Leu Glu Phe Val Ser Asn Ile Ala Lys Thr Phe Glu Ile Ser
385 390 395 400

Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg
405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala
420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp
435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser
450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp
465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile
485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met
500 505 510

Ala Ser Lys Pro Lys Glu Ser His Ala Phe Phe Thr Arg Glu Phe Thr
515 520 525

Gly Leu Glu Pro Ile Val Ser Asp Val Ile Arg Gly Ile Cys Arg Asp
530 535 540

Phe Leu Glu Ser Gln Gln
545 550

<210> 228

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide probe

<400> 228

tggtctcgca caccgatc

18

<210> 229

<211> 18

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 229
ctgctgtcca caggggag                                18

<210> 230
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 230
ccttgaagca tactgctc                                18

<210> 231
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 231
gagatagcaa tttccgcc                                18

<210> 232
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 232
ttcctcaaga gggcagcc                                18

<210> 233
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

<400> 233
cttggcacca atgtccgaga tttc                        24

<210> 234
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
        oligonucleotide probe

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 234
gctctgagga aggtgacgcg cggggcctcc gaacccttgg ccttg

45

<210> 235
<211> 2586
<212> DNA
<213> Homo sapiens

<400> 235
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gtcggggcgg cggctgcggg cgcagagcgg agatgcagcg gcttggggcc accctgctgt 180
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aaaaaa 2586

<210> 236
<211> 350
<212> PRT
<213> Homo sapiens

<400> 236
Met Gln Arg Leu Gly Ala Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala
1 5 10 15

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Pro Thr Ala₂₀ Pro Ala Pro Ala₂₅ Thr Ala Thr Ser Ala₃₀ Pro Val
Lys Pro Gly₃₅ Pro Ala Leu Ser Tyr₄₀ Pro Gln Glu Glu Ala₄₅ Thr Leu Asn
Glu Met₅₀ Phe Arg Glu Val₅₅ Glu Leu Met Glu Asp₆₀ Thr Gln His Lys
Leu Arg₆₅ Ser Ala Val₇₀ Glu Glu Met Glu Ala₇₅ Glu Glu Ala Ala Ala Lys₈₀
Ala Ser Ser Glu Val₈₅ Asn Leu Ala Asn Leu₉₀ Pro Pro Ser Tyr His₉₅ Asn
Glu Thr Asn Thr₁₀₀ Asp Thr Lys Val₁₀₅ Gly Asn Asn Thr Ile His₁₁₀ Val His
Arg Glu Ile₁₁₅ His Lys Ile Thr Asn₁₂₀ Asn Gln Thr Gly Gln₁₂₅ Met Val Phe
Ser Glu₁₃₀ Thr Val Ile Thr Ser₁₃₅ Val Gly Asp Glu Glu₁₄₀ Gly Arg Arg Ser
His Glu₁₄₅ Cys Ile Ile Asp₁₅₀ Glu Asp Cys Gly Pro₁₅₅ Ser Met Tyr Cys Gln₁₆₀
Phe Ala Ser Phe₁₆₅ Gln Tyr Thr Cys Gln Pro₁₇₀ Cys Arg Gly Gln Arg₁₇₅ Met
Leu Cys Thr Arg₁₈₀ Asp Ser Glu Cys Cys₁₈₅ Gly Asp Gln Leu Cys₁₉₀ Val Trp
Gly His Cys₁₉₅ Thr Lys Met Ala Thr₂₀₀ Arg Gly Ser Asn Gly₂₀₅ Thr Ile Cys
Asp Asn Gln Arg Asp Cys Gln₂₁₅ Pro Gly Leu Cys Cys₂₂₀ Ala Phe Gln Arg
Gly₂₂₅ Leu Leu Phe Pro Val₂₃₀ Cys Thr Pro Leu Pro₂₃₅ Val Glu Gly Glu Leu₂₄₀
Cys His Asp Pro₂₄₅ Ala Ser Arg Leu Leu Asp₂₅₀ Leu Ile Thr Trp Glu₂₅₅ Leu
Glu Pro Asp Gly₂₆₀ Ala Leu Asp Arg Cys₂₆₅ Pro Cys Ala Ser Gly₂₇₀ Leu Leu
Cys Gln Pro₂₇₅ His Ser His Ser Leu₂₈₀ Val Tyr Val Cys Lys₂₈₅ Pro Thr Phe
Val Gly₂₉₀ Ser Arg Asp Gln Asp₂₉₅ Gly Glu Ile Leu Leu₃₀₀ Pro Arg Glu Val
Pro Asp Glu Tyr Glu Val₃₁₀ Gly Ser Phe Met Glu₃₁₅ Glu Val Arg Gln Glu₃₂₀
Leu Glu Asp Leu₃₂₅ Glu Arg Ser Leu Thr Glu₃₃₀ Glu Met Ala Leu Gly₃₃₅ Glu
Pro Ala Ala Ala₃₄₀ Ala Ala Ala Leu Leu₃₄₅ Gly Gly Glu Glu Ile₃₅₀

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 237
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic oligonucleotide probe

 <400> 237
 ggagctgcac cccttgc 17

 <210> 238
 <211> 49
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic Oligonucleotide Probe

 <400> 238
 ggaggactgt gccaccatga gagactcttc aaaccaagg caaaattgg 49

 <210> 239
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic Oligonucleotide Probe

 <400> 239
 gcagagcgga gatgcagcgg cttg 24

 <210> 240
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic Oligonucleotide Probe

 <400> 240
 ttggcagctt catggagg 18

 <210> 241
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic Oligonucleotide Probe

 <400> 241
 cctgggcaaa aatgcaac 18

 <210> 242
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 242
ctccagctcc tggcgcacct cctc 24

<210> 243
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 243
ggctctcagc taccgcgag gagcgaggcc accctcaatg agatg 45

<210> 244
<211> 3679
<212> DNA
<213> Homo Sapien

<400> 244
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tctctctggg ctcagaagga ctctgaagat aacaataatt tcagcccatc 100
cactctcctt ccctcccaaa cacacatgtg catgtacaca cacacataca 150
cacacataca ctttcctctc cttcactgaa gactcacagt cactcactct 200
gtgagcaggt catagaaaag gacactaaag ccttaaggac aggcctggcc 250
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ggggtagata ctgcttctct gcaacctcct taactctgca tcctcttctt 650
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 aataaaaata aataataaca ataaaaaaa 3679

<210> 245

<211> 713

<212> PRT

<213> Homo Sapien

<400> 245

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Ala Thr Ala Thr Val Pro Val Val Pro Trp His Val Pro Cys Pro
 20 25 30

Pro Gln Cys Ala Cys Gln Ile Arg Pro Trp Tyr Thr Pro Arg Ser
 35 40 45

Ser Tyr Arg Glu Ala Thr Thr Val Asp Cys Asn Asp Leu Phe Leu
 50 55 60

Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu
 65 70 75

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Gln | Ser | Asn | Ser | Ile | Val | Arg | Val | Asp | Gln | Ser | Glu | Leu | Gly | 80 | 85 | 90 |
| Tyr | Leu | Ala | Asn | Leu | Thr | Glu | Leu | Asp | Leu | Ser | Gln | Asn | Ser | Phe | 95 | 100 | 105 |
| Ser | Asp | Ala | Arg | Asp | Cys | Asp | Phe | His | Ala | Leu | Pro | Gln | Leu | Leu | 110 | 115 | 120 |
| Ser | Leu | His | Leu | Glu | Glu | Asn | Gln | Leu | Thr | Arg | Leu | Glu | Asp | His | 125 | 130 | 135 |
| Ser | Phe | Ala | Gly | Leu | Ala | Ser | Leu | Gln | Glu | Leu | Tyr | Leu | Asn | His | 140 | 145 | 150 |
| Asn | Gln | Leu | Tyr | Arg | Ile | Ala | Pro | Arg | Ala | Phe | Ser | Gly | Leu | Ser | 155 | 160 | 165 |
| Asn | Leu | Leu | Arg | Leu | His | Leu | Asn | Ser | Asn | Leu | Leu | Arg | Ala | Ile | 170 | 175 | 180 |
| Asp | Ser | Arg | Trp | Phe | Glu | Met | Leu | Pro | Asn | Leu | Glu | Ile | Leu | Met | 185 | 190 | 195 |
| Ile | Gly | Gly | Asn | Lys | Val | Asp | Ala | Ile | Leu | Asp | Met | Asn | Phe | Arg | 200 | 205 | 210 |
| Pro | Leu | Ala | Asn | Leu | Arg | Ser | Leu | Val | Leu | Ala | Gly | Met | Asn | Leu | 215 | 220 | 225 |
| Arg | Glu | Ile | Ser | Asp | Tyr | Ala | Leu | Glu | Gly | Leu | Gln | Ser | Leu | Glu | 230 | 235 | 240 |
| Ser | Leu | Ser | Phe | Tyr | Asp | Asn | Gln | Leu | Ala | Arg | Val | Pro | Arg | Arg | 245 | 250 | 255 |
| Ala | Leu | Glu | Gln | Val | Pro | Gly | Leu | Lys | Phe | Leu | Asp | Leu | Asn | Lys | 260 | 265 | 270 |
| Asn | Pro | Leu | Gln | Arg | Val | Gly | Pro | Gly | Asp | Phe | Ala | Asn | Met | Leu | 275 | 280 | 285 |
| His | Leu | Lys | Glu | Leu | Gly | Leu | Asn | Asn | Met | Glu | Glu | Leu | Val | Ser | 290 | 295 | 300 |
| Ile | Asp | Lys | Phe | Ala | Leu | Val | Asn | Leu | Pro | Glu | Leu | Thr | Lys | Leu | 305 | 310 | 315 |
| Asp | Ile | Thr | Asn | Asn | Pro | Arg | Leu | Ser | Phe | Ile | His | Pro | Arg | Ala | 320 | 325 | 330 |
| Phe | His | His | Leu | Pro | Gln | Met | Glu | Thr | Leu | Met | Leu | Asn | Asn | Asn | 335 | 340 | 345 |
| Ala | Leu | Ser | Ala | Leu | His | Gln | Gln | Thr | Val | Glu | Ser | Leu | Pro | Asn | 350 | 355 | 360 |
| Leu | Gln | Glu | Val | Gly | Leu | His | Gly | Asn | Pro | Ile | Arg | Cys | Asp | Cys | 365 | 370 | 375 |
| Val | Ile | Arg | Trp | Ala | Asn | Ala | Thr | Gly | Thr | Arg | Val | Arg | Phe | Ile | 380 | 385 | 390 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Pro | Gln | Ser | Thr | Leu | Cys | Ala | Glu | Pro | Pro | Asp | Leu | Gln | Arg | 395 | 400 | 405 |
| Leu | Pro | Val | Arg | Glu | Val | Pro | Phe | Arg | Glu | Met | Thr | Asp | His | Cys | 410 | 415 | 420 |
| Leu | Pro | Leu | Ile | Ser | Pro | Arg | Ser | Phe | Pro | Pro | Ser | Leu | Gln | Val | 425 | 430 | 435 |
| Ala | Ser | Gly | Glu | Ser | Met | Val | Leu | His | Cys | Arg | Ala | Leu | Ala | Glu | 440 | 445 | 450 |
| Pro | Glu | Pro | Glu | Ile | Tyr | Trp | Val | Thr | Pro | Ala | Gly | Leu | Arg | Leu | 455 | 460 | 465 |
| Thr | Pro | Ala | His | Ala | Gly | Arg | Arg | Tyr | Arg | Val | Tyr | Pro | Glu | Gly | 470 | 475 | 480 |
| Thr | Leu | Glu | Leu | Arg | Arg | Val | Thr | Ala | Glu | Glu | Ala | Gly | Leu | Tyr | 485 | 490 | 495 |
| Thr | Cys | Val | Ala | Gln | Asn | Leu | Val | Gly | Ala | Asp | Thr | Lys | Thr | Val | 500 | 505 | 510 |
| Ser | Val | Val | Val | Gly | Arg | Ala | Leu | Leu | Gln | Pro | Gly | Arg | Asp | Glu | 515 | 520 | 525 |
| Gly | Gln | Gly | Leu | Glu | Leu | Arg | Val | Gln | Glu | Thr | His | Pro | Tyr | His | 530 | 535 | 540 |
| Ile | Leu | Leu | Ser | Trp | Val | Thr | Pro | Pro | Asn | Thr | Val | Ser | Thr | Asn | 545 | 550 | 555 |
| Leu | Thr | Trp | Ser | Ser | Ala | Ser | Ser | Leu | Arg | Gly | Gln | Gly | Ala | Thr | 560 | 565 | 570 |
| Ala | Leu | Ala | Arg | Leu | Pro | Arg | Gly | Thr | His | Ser | Tyr | Asn | Ile | Thr | 575 | 580 | 585 |
| Arg | Leu | Leu | Gln | Ala | Thr | Glu | Tyr | Trp | Ala | Cys | Leu | Gln | Val | Ala | 590 | 595 | 600 |
| Phe | Ala | Asp | Ala | His | Thr | Gln | Leu | Ala | Cys | Val | Trp | Ala | Arg | Thr | 605 | 610 | 615 |
| Lys | Glu | Ala | Thr | Ser | Cys | His | Arg | Ala | Leu | Gly | Asp | Arg | Pro | Gly | 620 | 625 | 630 |
| Leu | Ile | Ala | Ile | Leu | Ala | Leu | Ala | Val | Leu | Leu | Leu | Ala | Ala | Gly | 635 | 640 | 645 |
| Leu | Ala | Ala | His | Leu | Gly | Thr | Gly | Gln | Pro | Arg | Lys | Gly | Val | Gly | 650 | 655 | 660 |
| Gly | Arg | Arg | Pro | Leu | Pro | Pro | Ala | Trp | Ala | Phe | Trp | Gly | Trp | Ser | 665 | 670 | 675 |
| Ala | Pro | Ser | Val | Arg | Val | Val | Ser | Ala | Pro | Leu | Val | Leu | Pro | Trp | 680 | 685 | 690 |
| Asn | Pro | Gly | Arg | Lys | Leu | Pro | Arg | Ser | Ser | Glu | Gly | Glu | Thr | Leu | 695 | 700 | 705 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Leu Pro Pro Leu Ser Gln Asn Ser
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<210> 246

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 246

aacaaggtaa gatgcatcc tg 22

<210> 247

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 247

aaacttgctg atggagacca gctc 24

<210> 248

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 248

aggggctgca aagcctggag agcctctcct tctatgacaa ccagc 45

<210> 249

<211> 3401

<212> DNA

<213> Homo Sapien

<400> 249

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catcaagttc gacgtggact gcaccgtgga cattgagagc ctgacgggct 200

accgcaccta ccgctgtgcc caccctctgg ccacactctt caagatcctg 250

gcgtccttct acatcagcct agtcatcttc tacggcctca tctgcatgta 300

cacactgtgg tggatgctac ggcgctccct caagaagtac tcgtttgagt 350

cgatccgtga ggagagcagc tacagcgaca tccccgacgt caagaacgac 400

ttcgcccttca tgctgcacct cattgaccaa tacgacccgc tctactccaa 450

gcgcttcgcc gtcttctgt cggaggtgag tgagaacaag ctgcggcagc 500

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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a 3401

<210> 250

<211> 546

<212> PRT

<213> Homo Sapien

<400> 250

Met Arg Gln Thr Ile Ile Lys Val Ile Lys Phe Ile Leu Ile Ile

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | |
|---------------------|---------------------|-----------------|-----|
| 1 | 5 | 10 | 15 |
| Cys Tyr Thr Val Tyr | Tyr Val His Asn Ile | Lys Phe Asp Val | Asp |
| 20 | 25 | 30 | |
| Cys Thr Val Asp Ile | Glu Ser Leu Thr Gly | Tyr Arg Thr Tyr | Arg |
| 35 | 40 | 45 | |
| Cys Ala His Pro Leu | Ala Thr Leu Phe Lys | Ile Leu Ala Ser | Phe |
| 50 | 55 | 60 | |
| Tyr Ile Ser Leu Val | Ile Phe Tyr Gly Leu | Ile Cys Met Tyr | Thr |
| 65 | 70 | 75 | |
| Leu Trp Trp Met Leu | Arg Arg Ser Leu Lys | Lys Tyr Ser Phe | Glu |
| 80 | 85 | 90 | |
| Ser Ile Arg Glu Glu | Ser Ser Tyr Ser Asp | Ile Pro Asp Val | Lys |
| 95 | 100 | 105 | |
| Asn Asp Phe Ala Phe | Met Leu His Leu Ile | Asp Gln Tyr Asp | Pro |
| 110 | 115 | 120 | |
| Leu Tyr Ser Lys Arg | Phe Ala Val Phe Leu | Ser Glu Val Ser | Glu |
| 125 | 130 | 135 | |
| Asn Lys Leu Arg Gln | Leu Asn Leu Asn Asn | Glu Trp Thr Leu | Asp |
| 140 | 145 | 150 | |
| Lys Leu Arg Gln Arg | Leu Thr Lys Asn Ala | Gln Asp Lys Leu | Glu |
| 155 | 160 | 165 | |
| Leu His Leu Phe Met | Leu Ser Gly Ile Pro | Asp Thr Val Phe | Asp |
| 170 | 175 | 180 | |
| Leu Val Glu Leu Glu | Val Leu Lys Leu Glu | Leu Ile Pro Asp | Val |
| 185 | 190 | 195 | |
| Thr Ile Pro Pro Ser | Ile Ala Gln Leu Thr | Gly Leu Lys Glu | Leu |
| 200 | 205 | 210 | |
| Trp Leu Tyr His Thr | Ala Ala Lys Ile Glu | Ala Pro Ala Leu | Ala |
| 215 | 220 | 225 | |
| Phe Leu Arg Glu Asn | Leu Arg Ala Leu His | Ile Lys Phe Thr | Asp |
| 230 | 235 | 240 | |
| Ile Lys Glu Ile Pro | Leu Trp Ile Tyr Ser | Leu Lys Thr Leu | Glu |
| 245 | 250 | 255 | |
| Glu Leu His Leu Thr | Gly Asn Leu Ser Ala | Glu Asn Asn Arg | Tyr |
| 260 | 265 | 270 | |
| Ile Val Ile Asp Gly | Leu Arg Glu Leu Lys | Arg Leu Lys Val | Leu |
| 275 | 280 | 285 | |
| Arg Leu Lys Ser Asn | Leu Ser Lys Leu Pro | Gln Val Val Thr | Asp |
| 290 | 295 | 300 | |
| Val Gly Val His Leu | Gln Lys Leu Ser Ile | Asn Asn Glu Gly | Thr |
| 305 | 310 | 315 | |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Lys Leu Ile Val Leu Asn Ser Leu Lys Lys Met Ala Asn Leu Thr
 320 325 330

Glu Leu Glu Leu Ile Arg Cys Asp Leu Glu Arg Ile Pro His Ser
 335 340 345

Ile Phe Ser Leu His Asn Leu Gln Glu Ile Asp Leu Lys Asp Asn
 350 355 360

Asn Leu Lys Thr Ile Glu Glu Ile Ile Ser Phe Gln His Leu His
 365 370 375

Arg Leu Thr Cys Leu Lys Leu Trp Tyr Asn His Ile Ala Tyr Ile
 380 385 390

Pro Ile Gln Ile Gly Asn Leu Thr Asn Leu Glu Arg Leu Tyr Leu
 395 400 405

Asn Arg Asn Lys Ile Glu Lys Ile Pro Thr Gln Leu Phe Tyr Cys
 410 415 420

Arg Lys Leu Arg Tyr Leu Asp Leu Ser His Asn Asn Leu Thr Phe
 425 430 435

Leu Pro Ala Asp Ile Gly Leu Leu Gln Asn Leu Gln Asn Leu Ala
 440 445 450

Ile Thr Ala Asn Arg Ile Glu Thr Leu Pro Pro Glu Leu Phe Gln
 455 460 465

Cys Arg Lys Leu Arg Ala Leu His Leu Gly Asn Asn Val Leu Gln
 470 475 480

Ser Leu Pro Ser Arg Val Gly Glu Leu Thr Asn Leu Thr Gln Ile
 485 490 495

Glu Leu Arg Gly Asn Arg Leu Glu Cys Leu Pro Val Glu Leu Gly
 500 505 510

Glu Cys Pro Leu Leu Lys Arg Ser Gly Leu Val Val Glu Glu Asp
 515 520 525

Leu Phe Asn Thr Leu Pro Pro Glu Val Lys Glu Arg Leu Trp Arg
 530 535 540

Ala Asp Lys Glu Gln Ala
 545

<210> 251

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 251

caacaatgag ggcaccaagc 20

<210> 252

<211> 24

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Synthetic Oligonucleotide Probe

<400> 252

gatggctagg ttctggaggt tctg 24

<210> 253

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 253

caacctgcag gagattgacc tcaaggacaa caacctcaag accatcg 47

<210> 254

<211> 1650

<212> DNA

<213> Homo Sapien

<400> 254

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 ccagacagtt ccattctaca ttttctcaga gtcctatgga ggaaaaatgg 550
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 taactaaaag cactcccacg tctacaatgg agtcgagtct agaattcaca 900
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 tcgtagatac catgggctcag gaggcctggg tgcggaaact gaagtggcca 1200
 gaactgccta aattcagtca gctgaagtgg aaggccctgt acagtgaccc 1250
 taaatctttg gaaacatctg cttttgtcaa gtcctacaag aaccttgctt 1300
 tctactggat tctgaaagct ggtcatatgg ttccttctga ccaaggggac 1350
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 gggctggaga tgagctgggt tggccttggg gcacagagct gagctgaggc 1450
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<210> 255

<211> 452

<212> PRT

<213> Homo Sapien

<400> 255

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Glu | Leu | Ala | Leu | Arg | Arg | Ser | Pro | Val | Pro | Arg | Trp | Leu | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |
| Leu | Leu | Pro | Leu | Leu | Leu | Gly | Leu | Asn | Ala | Gly | Ala | Val | Ile | Asp |
| | | | 20 | | | | | | 25 | | | | | 30 |
| Trp | Pro | Thr | Glu | Glu | Gly | Lys | Glu | Val | Trp | Asp | Tyr | Val | Thr | Val |
| | | | 35 | | | | | | 40 | | | | | 45 |
| Arg | Lys | Asp | Ala | Tyr | Met | Phe | Trp | Trp | Leu | Tyr | Tyr | Ala | Thr | Asn |
| | | | 50 | | | | | | 55 | | | | | 60 |
| Ser | Cys | Lys | Asn | Phe | Ser | Glu | Leu | Pro | Leu | Val | Met | Trp | Leu | Gln |
| | | | 65 | | | | | | 70 | | | | | 75 |
| Gly | Gly | Pro | Gly | Gly | Ser | Ser | Thr | Gly | Phe | Gly | Asn | Phe | Glu | Glu |
| | | | 80 | | | | | | 85 | | | | | 90 |
| Ile | Gly | Pro | Leu | Asp | Ser | Asp | Leu | Lys | Pro | Arg | Lys | Thr | Thr | Trp |
| | | | 95 | | | | | | 100 | | | | | 105 |
| Leu | Gln | Ala | Ala | Ser | Leu | Leu | Phe | Val | Asp | Asn | Pro | Val | Gly | Thr |
| | | | 110 | | | | | | 115 | | | | | 120 |
| Gly | Phe | Ser | Tyr | Val | Asn | Gly | Ser | Gly | Ala | Tyr | Ala | Lys | Asp | Leu |
| | | | 125 | | | | | | 130 | | | | | 135 |
| Ala | Met | Val | Ala | Ser | Asp | Met | Met | Val | Leu | Leu | Lys | Thr | Phe | Phe |
| | | | 140 | | | | | | 145 | | | | | 150 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ser Cys His Lys Glu Phe Gln Thr Val Pro Phe Tyr Ile Phe Ser
 155 160 165
 Glu Ser Tyr Gly Gly Lys Met Ala Ala Gly Ile Gly Leu Glu Leu
 170 175 180
 Tyr Lys Ala Ile Gln Arg Gly Thr Ile Lys Cys Asn Phe Ala Gly
 185 190 195
 Val Ala Leu Gly Asp Ser Trp Ile Ser Pro Val Asp Ser Val Leu
 200 205 210
 Ser Trp Gly Pro Tyr Leu Tyr Ser Met Ser Leu Leu Glu Asp Lys
 215 220 225
 Gly Leu Ala Glu Val Ser Lys Val Ala Glu Gln Val Leu Asn Ala
 230 235 240
 Val Asn Lys Gly Leu Tyr Arg Glu Ala Thr Glu Leu Trp Gly Lys
 245 250 255
 Ala Glu Met Ile Ile Glu Gln Asn Thr Asp Gly Val Asn Phe Tyr
 260 265 270
 Asn Ile Leu Thr Lys Ser Thr Pro Thr Ser Thr Met Glu Ser Ser
 275 280 285
 Leu Glu Phe Thr Gln Ser His Leu Val Cys Leu Cys Gln Arg His
 290 295 300
 Val Arg His Leu Gln Arg Asp Ala Leu Ser Gln Leu Met Asn Gly
 305 310 315
 Pro Ile Arg Lys Lys Leu Lys Ile Ile Pro Glu Asp Gln Ser Trp
 320 325 330
 Gly Gly Gln Ala Thr Asn Val Phe Val Asn Met Glu Glu Asp Phe
 335 340 345
 Met Lys Pro Val Ile Ser Ile Val Asp Glu Leu Leu Glu Ala Gly
 350 355 360
 Ile Asn Val Thr Val Tyr Asn Gly Gln Leu Asp Leu Ile Val Asp
 365 370 375
 Thr Met Gly Gln Glu Ala Trp Val Arg Lys Leu Lys Trp Pro Glu
 380 385 390
 Leu Pro Lys Phe Ser Gln Leu Lys Trp Lys Ala Leu Tyr Ser Asp
 395 400 405
 Pro Lys Ser Leu Glu Thr Ser Ala Phe Val Lys Ser Tyr Lys Asn
 410 415 420
 Leu Ala Phe Tyr Trp Ile Leu Lys Ala Gly His Met Val Pro Ser
 425 430 435
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 440 445 450

Gln Glu

<210> 256

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttgccc gtggcagggg agcctgcgcc 200
tgtgggattc ccacgtatgc ggagtgaacc tgctcagcca ccgctgggca 250
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ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550
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tcaggctgcc atcataaaca actctatgtg caaccacctc ttcctcaagt 650
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gctgtggtcg gccaatcgg cccggtgtct acaccaatat cagccaccac 850
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tggggccggt ctgagcctac ctgagcccat gcagcctggg gccactgcca 1000
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<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

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Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Ala Arg
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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser
          20          25          30
Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
50 55 60
Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg
65 70 75
Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr Ser Asp Leu
80 85 90
Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser
95 100 105
Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe
110 115 120
Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro
125 130 135
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
140 145 150
Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe
155 160 165
Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys
170 175 180
Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln
185 190 195
Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys
200 205 210
Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly
215 220 225
Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
230 235 240
Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val
245 250 255
Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val
260 265 270
Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met
275 280 285
Ala Gln Ser Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu
290 295 300
Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
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<210> 258
<211> 2427
<212> DNA
<213> Homo Sapien

<400> 258
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Page 133

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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<210> 259
<211> 556
<212> PRT
<213> Homo Sapien

<400> 259
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20 25 30
Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu
35 40 45
Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg
50 55 60
Leu Ser Glu Leu Val Gln Ala Val Ser Asp Pro Ser Ser Pro Gln
65 70 75
Tyr Gly Lys Tyr Leu Thr Leu Glu Asn Val Ala Asp Leu Val Arg
80 85 90
Pro Ser Pro Leu Thr Leu His Thr Val Gln Lys Trp Leu Leu Ala
95 100 105
Ala Gly Ala Gln Lys Cys His Ser Val Ile Thr Gln Asp Phe Leu
110 115 120

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | |
|-----------------|---------|-----------------|---------|-----------------|---------|
| Thr Cys Trp Leu | Ser 125 | Ile Arg Gln Ala | Glu 130 | Leu Leu Leu Pro | Gly 135 |
| Ala Glu Phe His | His 140 | Tyr Val Gly Gly | Pro 145 | Thr Glu Thr His | Val 150 |
| Val Arg Ser Pro | His 155 | Pro Tyr Gln Leu | Pro 160 | Gln Ala Leu Ala | Pro 165 |
| His Val Asp Phe | Val 170 | Gly Gly Leu His | Arg 175 | Phe Pro Pro Thr | Ser 180 |
| Ser Leu Arg Gln | Arg 185 | Pro Glu Pro Gln | Val 190 | Thr Gly Thr Val | Gly 195 |
| Leu His Leu Gly | Val 200 | Thr Pro Ser Val | Ile 205 | Arg Lys Arg Tyr | Asn 210 |
| Leu Thr Ser Gln | Asp 215 | Val Gly Ser Gly | Thr 220 | Ser Asn Asn Ser | Gln 225 |
| Ala Cys Ala Gln | Phe 230 | Leu Glu Gln Tyr | Phe 235 | His Asp Ser Asp | Leu 240 |
| Ala Gln Phe Met | Arg 245 | Leu Phe Gly Gly | Asn 250 | Phe Ala His Gln | Ala 255 |
| Ser Val Ala Arg | Val 260 | Val Gly Gln Gln | Gly 265 | Arg Gly Arg Ala | Gly 270 |
| Ile Glu Ala Ser | Leu 275 | Asp Val Gln Tyr | Leu 280 | Met Ser Ala Gly | Ala 285 |
| Asn Ile Ser Thr | Trp 290 | Val Tyr Ser Ser | Pro 295 | Gly Arg His Glu | Gly 300 |
| Gln Glu Pro Phe | Leu 305 | Gln Trp Leu Met | Leu 310 | Leu Ser Asn Glu | Ser 315 |
| Ala Leu Pro His | Val 320 | His Thr Val Ser | Tyr 325 | Gly Asp Asp Glu | Asp 330 |
| Ser Leu Ser Ser | Ala 335 | Tyr Ile Gln Arg | Val 340 | Asn Thr Glu Leu | Met 345 |
| Lys Ala Ala Ala | Arg 350 | Gly Leu Thr Leu | Leu 355 | Phe Ala Ser Gly | Asp 360 |
| Ser Gly Ala Gly | Cys 365 | Trp Ser Val Ser | Gly 370 | Arg His Gln Phe | Arg 375 |
| Pro Thr Phe Pro | Ala 380 | Ser Ser Pro Tyr | Val 385 | Thr Thr Val Gly | Gly 390 |
| Thr Ser Phe Gln | Glu 395 | Pro Phe Leu Ile | Thr 400 | Asn Glu Ile Val | Asp 405 |
| Tyr Ile Ser Gly | Gly 410 | Gly Phe Ser Asn | Val 415 | Phe Pro Arg Pro | Ser 420 |
| Tyr Gln Glu Glu | Ala 425 | Val Thr Lys Phe | Leu 430 | Ser Ser Ser Pro | His 435 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Pro | Pro | Ser | Leu | Tyr | Phe | Asn | Ala | Ser | Gly | Arg | Ala | Tyr | Pro |
| | | | 440 | | | | | | 445 | | | | | 450 |
| Asp | Val | Ala | Ala | Leu | Ser | Asp | Gly | Tyr | Trp | Val | Val | Ser | Asn | Arg |
| | | | 455 | | | | | | 460 | | | | | 465 |
| Val | Pro | Ile | Pro | Trp | Val | Ser | Gly | Thr | Ser | Ala | Ser | Thr | Pro | Val |
| | | | 470 | | | | | | 475 | | | | | 480 |
| Phe | Gly | Gly | Ile | Leu | Ser | Leu | Ile | Asn | Glu | His | Arg | Ile | Leu | Ser |
| | | | 485 | | | | | | 490 | | | | | 495 |
| Gly | Arg | Pro | Pro | Leu | Gly | Phe | Leu | Asn | Pro | Arg | Leu | Tyr | Gln | Gln |
| | | | 500 | | | | | | 505 | | | | | 510 |
| His | Gly | Ala | Gly | Leu | Phe | Asp | Val | Thr | Arg | Gly | Cys | His | Glu | Ser |
| | | | 515 | | | | | | 520 | | | | | 525 |
| Cys | Leu | Asp | Glu | Glu | Val | Glu | Gly | Gln | Gly | Phe | Cys | Ser | Gly | Pro |
| | | | 530 | | | | | | 535 | | | | | 540 |
| Gly | Trp | Asp | Pro | Val | Thr | Gly | Trp | Gly | Thr | Pro | Thr | Ser | Gln | Leu |
| | | | 545 | | | | | | 550 | | | | | 555 |

Cys

<210> 260
 <211> 1638
 <212> DNA
 <213> Homo Sapien

<400> 260
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 attccagggc tcctcttctt tctcttcttt ctgctctgtg ctgttgggca 150
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 tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250
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 atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400
 tacatcctca gcagtagtgg agatggggcc caacaccgag actcaggggtc 450
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 tcagcatttt tgggaaggac ttctgtctca actacccttt ctcaacatca 550
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 cccagaagct tcgagtgggc ttcctaaagc ccaagtttaa agatggtggt 700
 cgagggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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 atatttggca tacaagagat atgaaaaaaaa aaaaaaaaa 1638

<210> 261
 <211> 383
 <212> PRT
 <213> Homo Sapien

<400> 261
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 20 25 30
 Thr Trp Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr
 35 40 45
 Leu Asn Leu Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu
 50 55 60
 Val Ser Ser Ser Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu
 65 70 75
 Pro Thr Tyr Glu Glu Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu
 80 85 90
 Tyr Ala Asn Gly Ser Arg Thr Glu Thr Gln Val Gly Ile Tyr Ile
 95 100 105

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | |
|-----------------|---------|-----------------|---------|-----------------|---------|
| Leu Ser Ser Ser | Gly 110 | Asp Gly Ala Gln | His 115 | Arg Asp Ser Gly | Ser 120 |
| Ser Gly Lys Ser | Arg 125 | Arg Lys Arg Gln | Ile 130 | Tyr Gly Tyr Asp | Ser 135 |
| Arg Phe Ser Ile | Phe 140 | Gly Lys Asp Phe | Leu 145 | Leu Asn Tyr Pro | Phe 150 |
| Ser Thr Ser Val | Lys 155 | Leu Ser Thr Gly | Cys 160 | Thr Gly Thr Leu | Val 165 |
| Ala Glu Lys His | Val 170 | Leu Thr Ala Ala | His 175 | Cys Ile His Asp | Gly 180 |
| Lys Thr Tyr Val | Lys 185 | Gly Thr Gln Lys | Leu 190 | Arg Val Gly Phe | Leu 195 |
| Lys Pro Lys Phe | Lys 200 | Asp Gly Gly Arg | Gly 205 | Ala Asn Asp Ser | Thr 210 |
| Ser Ala Met Pro | Glu 215 | Gln Met Lys Phe | Gln 220 | Trp Ile Arg Val | Lys 225 |
| Arg Thr His Val | Pro 230 | Lys Gly Trp Ile | Lys 235 | Gly Asn Ala Asn | Asp 240 |
| Ile Gly Met Asp | Tyr 245 | Asp Tyr Ala Leu | Leu 250 | Glu Leu Lys Lys | Pro 255 |
| His Lys Arg Lys | Phe 260 | Met Lys Ile Gly | Val 265 | Ser Pro Pro Ala | Lys 270 |
| Gln Leu Pro Gly | Gly 275 | Arg Ile His Phe | Ser 280 | Gly Tyr Asp Asn | Asp 285 |
| Arg Pro Gly Asn | Leu 290 | Val Tyr Arg Phe | Cys 295 | Asp Val Lys Asp | Glu 300 |
| Thr Tyr Asp Leu | Leu 305 | Tyr Gln Gln Cys | Asp 310 | Ala Gln Pro Gly | Ala 315 |
| Ser Gly Ser Gly | Val 320 | Tyr Val Arg Met | Trp 325 | Lys Arg Gln Gln | Gln 330 |
| Lys Trp Glu Arg | Lys 335 | Ile Ile Gly Ile | Phe 340 | Ser Gly His Gln | Trp 345 |
| Val Asp Met Asn | Gly 350 | Ser Pro Gln Asp | Phe 355 | Asn Val Ala Val | Arg 360 |
| Ile Thr Pro Leu | Lys 365 | Tyr Ala Gln Ile | Cys 370 | Tyr Trp Ile Lys | Gly 375 |
| Asn Tyr Leu Asp | Cys 380 | Arg Glu Gly | | | |

<210> 262
 <211> 1378
 <212> DNA
 <213> Homo Sapien

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 262
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ccatggtggt ttctggagcg cccccagccc tgggtggggg ctgtctcggc 100
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caggatacct gttccccag cctgtgggaa gccccagcag ctgaaccggg 200
ttgtgggcgg cgaggacagc actgacagcg agtggccctg gatcgtgagc 250
atccagaaga atgggaccca cactgcgca ggttctctgc tcaccagccg 300
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acctgttctc tgtgctgctg ggggcctggc agctggggaa ccctggctct 400
cgggtcccaga aggtgggtgt tgcctgggtg gagccccacc ctgtgtattc 450
ctggaaggaa ggtgcctgtg cagacattgc cctggtgctg ctcgagcgct 500
ccatacagtt ctcagagcgg gtcctgccc tctgcctacc tgatgcctct 550
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ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800
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tcctagggcg cagcgggacg cggggctcgg atctgaaagg cggccagatc 1050
cacatctgga tctggatctg cggcggcctc gggcggtttc ccccgccgta 1100
aataggctca tctacctta cctctggggg cccggacggc tgctgcggaa 1150
aggaaacccc ctccccgacc cgcccagcgg cctcaggccc ccctccaagg 1200
catcaggccc cgcccaacgg cctcatgtcc ccgccccac gacttccggc 1250
cccgcccccg ggccccagcg cttttgtgta tataaatgtt aatgattttt 1300
ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350
ataaattatt tattctcaa aaaaaaaa 1378

<210> 263
<211> 317
<212> PRT
<213> Homo Sapien

<400> 263

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu
          20          25          30
Asn Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln
          35          40          45
Gln Leu Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu
          50          55          60
Trp Pro Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys
          65          70          75
Ala Gly Ser Leu Leu Thr Ser Arg Trp Val Ile Thr Ala Ala His
          80          85          90
Cys Phe Lys Asp Asn Leu Asn Lys Pro Tyr Leu Phe Ser Val Leu
          95          100          105
Leu Gly Ala Trp Gln Leu Gly Asn Pro Gly Ser Arg Ser Gln Lys
          110          115          120
Val Gly Val Ala Trp Val Glu Pro His Pro Val Tyr Ser Trp Lys
          125          130          135
Glu Gly Ala Cys Ala Asp Ile Ala Leu Val Arg Leu Glu Arg Ser
          140          145          150
Ile Gln Phe Ser Glu Arg Val Leu Pro Ile Cys Leu Pro Asp Ala
          155          160          165
Ser Ile His Leu Pro Pro Asn Thr His Cys Trp Ile Ser Gly Trp
          170          175          180
Gly Ser Ile Gln Asp Gly Val Pro Leu Pro His Pro Gln Thr Leu
          185          190          195
Gln Lys Leu Lys Val Pro Ile Ile Asp Ser Glu Val Cys Ser His
          200          205          210
Leu Tyr Trp Arg Gly Ala Gly Gln Gly Pro Ile Thr Glu Asp Met
          215          220          225
Leu Cys Ala Gly Tyr Leu Glu Gly Glu Arg Asp Ala Cys Leu Gly
          230          235          240
Asp Ser Gly Gly Pro Leu Met Cys Gln Val Asp Gly Ala Trp Leu
          245          250          255
Leu Ala Gly Ile Ile Ser Trp Gly Glu Gly Cys Ala Glu Arg Asn
          260          265          270
Arg Pro Gly Val Tyr Ile Ser Leu Ser Ala His Arg Ser Trp Val
          275          280          285
Glu Lys Ile Val Gln Gly Val Gln Leu Arg Gly Arg Ala Gln Gly
          290          295          300
Gly Gly Ala Leu Arg Ala Pro Ser Gln Gly Ser Gly Ala Ala Ala
          305          310          315

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Arg Ser

<210> 264

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 264

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<210> 265

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 265

gcagagggtgt ctaagggtg 19

<210> 266

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 266

agctctagac caatgccagc ttcc 24

<210> 267

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 267

gccaccaact cctgcaagaa cttctcagaa ctgcccctgg tcatg 45

<210> 268

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 268

ggggaattca ccctatgaca ttgcc 25

<210> 269

<211> 24

<212> DNA

<213> Artificial Sequence

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

<223> Synthetic Oligonucleotide Probe

<400> 269

gaatgccctg caagcatcaa ctgg 24

<210> 270

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 270

gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50

<210> 271

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 271

gcggaagggc agaatgggac tccaag 26

<210> 272

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 272

cagccctgcc acatgtgc 18

<210> 273

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 273

tactgggtgg tcagcaac 18

<210> 274

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 274

ggcgaagagc agggtgagac cccg 24

<210> 275

<211> 45

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 275
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<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 276
gggcagggat tccagggtc c 21

<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 277
ggctatgaca gcaggttc 18

<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 278
tgacaatgac cgaccagg 18

<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 279
gcatcgatt gctggtagag caag 24

<210> 280
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 280

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
ttacagtgcc ccctggaac ccacttggcc tgcataccgc ctccc 45

<210> 281

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 281

cgtctcgagc gtcataca gttcccttgc ccca 34

<210> 282

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 282

tggaggggga gcgggatgct tgtctgggcg actccggggg ccccctcatg 50

tgccaggtgg a 61

<210> 283

<211> 119

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 283

ccctcagacc ctgcagaagc tgaaggttcc tatcatcgac tcggaagtct 50

gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100

atgctgtgtg ccggctact 119

<210> 284

<211> 1875

<212> DNA

<213> Homo Sapien

<400> 284

gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50

ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100

agatgaggag aaacgtttga tgggtggagct gcacaacctc taccggggccc 150

aggtatcccc gacggcctca gacatgctgc acatgagatg ggacgaggag 200

ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250

caaggagcgc gggcgccgcg gcgagaatct gttcgccatc acagacgagg 300

gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350

tacaacctca gcgccgccac ctgcagccca ggccagatgt gcggccacta 400

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cacgcaggtg gtatggggcca agacagagag gatcggctgt ggttcccact 450
 tctgtgagaa gctccaggggt gttgaggaga ccaacatcga attactggtg 500
 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550
 ggggactccg tgctcccaat gtccctcttg ctaccactgc aagaactccc 600
 tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650
 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700
 aatgggtact ctttcttccc tagcaacggg gattccggct ttcttggtaa 750
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 gttcctatcc caaaatcagc agacaaagt acagacaaaa caaaagtgcc 1000
 ctctaggagc ccagagaact ctctggacct caagatgtcc ctgacagggg 1050
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 ataaaaacct gtccaacctg tgaaa 1875

<210> 285

<211> 463

<212> PRT

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Homo Sapien

<400> 285

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Met His Gly Ser Cys Ser Phe Leu Met Leu Leu Leu Pro Leu Leu
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Leu Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp
          20          25          30
Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala
          35          40          45
Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp
          50          55          60
Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val
          65          70          75
Trp Gly His Asn Lys Glu Arg Gly Arg Arg Gly Glu Asn Leu Phe
          80          85          90
Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu
          95          100          105
Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys
          110          115          120
Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala
          125          130          135
Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu
          140          145          150
Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr
          155          160          165
Glu Pro Pro Gly Asn Val Lys Gly Lys Arg Pro Tyr Gln Glu Gly
          170          175          180
Thr Pro Cys Ser Gln Cys Pro Ser Gly Tyr His Cys Lys Asn Ser
          185          190          195
Leu Cys Glu Pro Ile Gly Ser Pro Glu Asp Ala Gln Asp Leu Pro
          200          205          210
Tyr Leu Val Thr Glu Ala Pro Ser Phe Arg Ala Thr Glu Ala Ser
          215          220          225
Asp Ser Arg Lys Met Gly Thr Pro Ser Ser Leu Ala Thr Gly Ile
          230          235          240
Pro Ala Phe Leu Val Thr Glu Val Ser Gly Ser Leu Ala Thr Lys
          245          250          255
Ala Leu Pro Ala Val Glu Thr Gln Ala Pro Thr Ser Leu Ala Thr
          260          265          270
Lys Asp Pro Pro Ser Met Ala Thr Glu Ala Pro Pro Cys Val Thr
          275          280          285
Thr Glu Val Pro Ser Ile Leu Ala Ala His Ser Leu Pro Ser Leu
          290          295          300

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Asp Glu Glu Pro Val Thr Phe Pro Lys Ser Thr His Val Pro Ile
305 310 315

Pro Lys Ser Ala Asp Lys Val Thr Asp Lys Thr Lys Val Pro Ser
320 325 330

Arg Ser Pro Glu Asn Ser Leu Asp Pro Lys Met Ser Leu Thr Gly
335 340 345

Ala Arg Glu Leu Leu Pro His Ala Gln Glu Glu Ala Glu Ala Glu
350 355 360

Ala Glu Leu Pro Pro Ser Ser Glu Val Leu Ala Ser Val Phe Pro
365 370 375

Ala Gln Asp Lys Pro Gly Glu Leu Gln Ala Thr Leu Asp His Thr
380 385 390

Gly His Thr Ser Ser Lys Ser Leu Pro Asn Phe Pro Asn Thr Ser
395 400 405

Ala Thr Ala Asn Ala Thr Gly Gly Arg Ala Leu Ala Leu Gln Ser
410 415 420

Ser Leu Pro Gly Ala Glu Gly Pro Asp Lys Pro Ser Val Val Ser
425 430 435

Gly Leu Asn Ser Gly Pro Gly His Val Trp Gly Pro Leu Leu Gly
440 445 450

Leu Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe
455 460

<210> 286

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide Probe

<400> 286

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<210> 287

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide Probe

<400> 287

ctcatattgc acaccagtaa ttcg 24

<210> 288

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 288
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<210> 289

<211> 3662

<212> DNA

<213> Homo Sapien

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gcccacctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 gccagcagca gtgattcccc aatgactttt gcttgaaaaa aagacaatga 1500
 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggccaag 1550
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 tcttccccag acttggactc tgggtcagag gaagatggga aagaaaggac 3150
 agattttcag gaagaaaadc acatttgtac ctttaaacag acttttagaaa 3200
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 tgtcaatttg aa 3662

<210> 290
 <211> 1059
 <212> PRT
 <213> Homo Sapien

<400> 290
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 1 5 10 15
 Ile Ser Arg Pro Asp Leu Ser His Asn Arg Leu Ser Phe Ile Lys
 20 25 30
 Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu
 35 40 45
 Asn Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
 50 55 60
 Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
 65 70 75
 Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu
 80 85 90
 Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro
 95 100 105
 Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr
 110 115 120
 Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu
 125 130 135

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Lys | Leu | Asn | Arg | Asn | Arg | Ile | Ser | Ala | Ile | Pro | Pro | Lys | 140 | 145 | 150 |
| Met | Phe | Lys | Leu | Pro | Gln | Leu | Gln | His | Leu | Glu | Leu | Asn | Arg | Asn | 155 | 160 | 165 |
| Lys | Ile | Lys | Asn | Val | Asp | Gly | Leu | Thr | Phe | Gln | Gly | Leu | Gly | Ala | 170 | 175 | 180 |
| Leu | Lys | Ser | Leu | Lys | Met | Gln | Arg | Asn | Gly | Val | Thr | Lys | Leu | Met | 185 | 190 | 195 |
| Asp | Gly | Ala | Phe | Trp | Gly | Leu | Ser | Asn | Met | Glu | Ile | Leu | Gln | Leu | 200 | 205 | 210 |
| Asp | His | Asn | Asn | Leu | Thr | Glu | Ile | Thr | Lys | Gly | Trp | Leu | Tyr | Gly | 215 | 220 | 225 |
| Leu | Leu | Met | Leu | Gln | Glu | Leu | His | Leu | Ser | Gln | Asn | Ala | Ile | Asn | 230 | 235 | 240 |
| Arg | Ile | Ser | Pro | Asp | Ala | Trp | Glu | Phe | Cys | Gln | Lys | Leu | Ser | Glu | 245 | 250 | 255 |
| Leu | Asp | Leu | Thr | Phe | Asn | His | Leu | Ser | Arg | Leu | Asp | Asp | Ser | Ser | 260 | 265 | 270 |
| Phe | Leu | Gly | Leu | Ser | Leu | Leu | Asn | Thr | Leu | His | Ile | Gly | Asn | Asn | 275 | 280 | 285 |
| Arg | Val | Ser | Tyr | Ile | Ala | Asp | Cys | Ala | Phe | Arg | Gly | Leu | Ser | Ser | 290 | 295 | 300 |
| Leu | Lys | Thr | Leu | Asp | Leu | Lys | Asn | Asn | Glu | Ile | Ser | Trp | Thr | Ile | 305 | 310 | 315 |
| Glu | Asp | Met | Asn | Gly | Ala | Phe | Ser | Gly | Leu | Asp | Lys | Leu | Arg | Arg | 320 | 325 | 330 |
| Leu | Ile | Leu | Gln | Gly | Asn | Arg | Ile | Arg | Ser | Ile | Thr | Lys | Lys | Ala | 335 | 340 | 345 |
| Phe | Thr | Gly | Leu | Asp | Ala | Leu | Glu | His | Leu | Asp | Leu | Ser | Asp | Asn | 350 | 355 | 360 |
| Ala | Ile | Met | Ser | Leu | Gln | Gly | Asn | Ala | Phe | Ser | Gln | Met | Lys | Lys | 365 | 370 | 375 |
| Leu | Gln | Gln | Leu | His | Leu | Asn | Thr | Ser | Ser | Leu | Leu | Cys | Asp | Cys | 380 | 385 | 390 |
| Gln | Leu | Lys | Trp | Leu | Pro | Gln | Trp | Val | Ala | Glu | Asn | Asn | Phe | Gln | 395 | 400 | 405 |
| Ser | Phe | Val | Asn | Ala | Ser | Cys | Ala | His | Pro | Gln | Leu | Leu | Lys | Gly | 410 | 415 | 420 |
| Arg | Ser | Ile | Phe | Ala | Val | Ser | Pro | Asp | Gly | Phe | Val | Cys | Asp | Asp | 425 | 430 | 435 |
| Phe | Pro | Lys | Pro | Gln | Ile | Thr | Val | Gln | Pro | Glu | Thr | Gln | Ser | Ala | | | |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | |
|-------------------------------------|-----|---------------------|-----|-----------------|-----|
| Ile Lys Gly Ser | Asn | Leu Ser Phe Ile | Cys | Ser Ala Ala Ser | Ser |
| | 445 | | 445 | | 450 |
| Ser Asp Ser Pro Met Thr Phe Ala Trp | | Lys Lys Asp Asn Glu | Leu | | |
| | 470 | | 475 | | 480 |
| Leu His Asp Ala Glu Met Glu Asn Tyr | | Ala His Leu Arg Ala | Gln | | |
| | 485 | | 490 | | 495 |
| Gly Gly Glu Val Met Glu Tyr Thr Thr | | Ile Leu Arg Leu Arg | Glu | | |
| | 500 | | 505 | | 510 |
| Val Glu Phe Ala Ser Glu Gly Lys Tyr | | Gln Cys Val Ile Ser | Asn | | |
| | 515 | | 520 | | 525 |
| His Phe Gly Ser Ser Tyr Ser Val Lys | | Ala Lys Leu Thr Val | Asn | | |
| | 530 | | 535 | | 540 |
| Met Leu Pro Ser Phe Thr Lys Thr Pro | | Met Asp Leu Thr Ile | Arg | | |
| | 545 | | 550 | | 555 |
| Ala Gly Ala Met Ala Arg Leu Glu Cys | | Ala Ala Val Gly His | Pro | | |
| | 560 | | 565 | | 570 |
| Ala Pro Gln Ile Ala Trp Gln Lys Asp | | Gly Gly Thr Asp Phe | Pro | | |
| | 575 | | 580 | | 585 |
| Ala Ala Arg Glu Arg Arg Met His Val | | Met Pro Glu Asp Asp | Val | | |
| | 590 | | 595 | | 600 |
| Phe Phe Ile Val Asp Val Lys Ile Glu | | Asp Ile Gly Val Tyr | Ser | | |
| | 605 | | 610 | | 615 |
| Cys Thr Ala Gln Asn Ser Ala Gly Ser | | Ile Ser Ala Asn Ala | Thr | | |
| | 620 | | 625 | | 630 |
| Leu Thr Val Leu Glu Thr Pro Ser Phe | | Leu Arg Pro Leu Leu | Asp | | |
| | 635 | | 640 | | 645 |
| Arg Thr Val Thr Lys Gly Glu Thr Ala | | Val Leu Gln Cys Ile | Ala | | |
| | 650 | | 655 | | 660 |
| Gly Gly Ser Pro Pro Pro Lys Leu Asn | | Trp Thr Lys Asp Asp | Ser | | |
| | 665 | | 670 | | 675 |
| Pro Leu Val Val Thr Glu Arg His Phe | | Phe Ala Ala Gly Asn | Gln | | |
| | 680 | | 685 | | 690 |
| Leu Leu Ile Ile Val Asp Ser Asp Val | | Ser Asp Ala Gly Lys | Tyr | | |
| | 695 | | 700 | | 705 |
| Thr Cys Glu Met Ser Asn Thr Leu Gly | | Thr Glu Arg Gly Asn | Val | | |
| | 710 | | 715 | | 720 |
| Arg Leu Ser Val Ile Pro Thr Pro Thr | | Cys Asp Ser Pro Gln | Met | | |
| | 725 | | 730 | | 735 |
| Thr Ala Pro Ser Leu Asp Asp Asp Gly | | Trp Ala Thr Val Gly | Val | | |
| | 740 | | 745 | | 750 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Val Ile Ile Ala Val Val Cys Cys Val Val Gly Thr Ser Leu Val
 755 760 765
 Trp Val Val Ile Ile Tyr His Thr Arg Arg Arg Asn Glu Asp Cys
 770 775 780
 Ser Ile Thr Asn Thr Asp Glu Thr Asn Leu Pro Ala Asp Ile Pro
 785 790 795
 Ser Tyr Leu Ser Ser Gln Gly Thr Leu Ala Asp Arg Gln Asp Gly
 800 805 810
 Tyr Val Ser Ser Glu Ser Gly Ser His His Gln Phe Val Thr Ser
 815 820 825
 Ser Gly Ala Gly Phe Phe Leu Pro Gln His Asp Ser Ser Gly Thr
 830 835 840
 Cys His Ile Asp Asn Ser Ser Glu Ala Asp Val Glu Ala Ala Thr
 845 850 855
 Asp Leu Phe Leu Cys Pro Phe Leu Gly Ser Thr Gly Pro Met Tyr
 860 865 870
 Leu Lys Gly Asn Val Tyr Gly Ser Asp Pro Phe Glu Thr Tyr His
 875 880 885
 Thr Gly Cys Ser Pro Asp Pro Arg Thr Val Leu Met Asp His Tyr
 890 895 900
 Glu Pro Ser Tyr Ile Lys Lys Lys Glu Cys Tyr Pro Cys Ser His
 905 910 915
 Pro Ser Glu Glu Ser Cys Glu Arg Ser Phe Ser Asn Ile Ser Trp
 920 925 930
 Pro Ser His Val Arg Lys Leu Leu Asn Thr Ser Tyr Ser His Asn
 935 940 945
 Glu Gly Pro Gly Met Lys Asn Leu Cys Leu Asn Lys Ser Ser Leu
 950 955 960
 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
 965 970 975
 Ser Phe Met Gly Thr Phe Gly Lys Ala Leu Arg Arg Pro His Leu
 980 985 990
 Asp Ala Tyr Ser Ser Phe Gly Gln Pro Ser Asp Cys Gln Pro Arg
 995 1000 1005
 Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
 1010 1015 1020
 Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn
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 His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro
 1040 1045 1050
 Asn Phe Gln Ser Tyr Asp Leu Asp Thr
 1055

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 <211> 2906
 <212> DNA
 <213> Homo Sapien

<400> 291
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 tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150
 gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
 acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250
 ttggtgtggt ctgacataaa taaataatct taaagcagct gttcccctcc 300
 ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcacia 350
 agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
 gatatttttg gaatgaaaag tttggggctt ttttagtaaa gtaaagaact 450
 ggtgtggtgg tgttttcctt tctttttgaa tttcccacia gaggagagga 500
 aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550
 gcagattgag gcattgattg ggggagagaa accagcagag cacagttaga 600
 tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650
 ttcacaaacc tccttttttt taaattttta ttccttttgg tatcaagatc 700
 atgcgttttc tcttgttcct aaccacctgg atttccatct ggatgttgct 750
 gtgatcagtc tgaaatacaa ctgtttgaat tccagaagga ccaacaccag 800
 ataaattatg aatgttgaac aagatgacct tacatccaca gcagataatg 850
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 gctggctctt caacttcttg tgggtggctgg tctggtgcgg gctcagacct 950
 gcccttctgt gtgctcctgc agcaaccagt tcagcaaggt gatttgtggt 1000
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 tgtctaaact gaaggagctc tggttgcgaa acaaccccat tgaaagcatc 1300
 ccttcttatg cttttaacag aattccttct ttgcgccgac tagacttagg 1350
 ggaattgaaa agactttcat acatctcaga aggtgccttt gaaggtctgt 1400

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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gacaaccttc agtcactagt ggagatcaac ctggcacaca ataatctaac 1650
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atttacatca caacccttgg aactgtaact gtgacatact gtggctcagc 1750
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taacactcct cccaatctaa aggggaggta cattggagag ctcgaccaga 1850
attacttcac atgctatgct ccggtgattg tggagccccc tgcagacctc 1900
aatgtcactg aaggcatggc agctgagctg aaatgtcggg cctccacatc 1950
cctgacatct gtatcttggg ttactccaaa tggaacagtc atgacacatg 2000
gggcgtacaa agtgcgagata gctgtgctca gtgatggtag gttaaatttc 2050
acaaatgtaa ctgtgcaaga tacaggcatg tacacatgta tggtgagtaa 2100
ttccgttggg aatactactg cttcagccac cctgaatggt actgcagcaa 2150
ccactactcc tttctcttac ttttcaaccg tcacagtaga gactatggaa 2200
ccgtctcagg atgaggcacg gaccacagat aacaatgtgg gtcccactcc 2250
agtggtcgac tgggagacca ccaatgtgac cacctctctc acaccacaga 2300
gcacaaggtc gacagagaaa accttcacca tcccagtgac tgatataaac 2350
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aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550
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caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800
tgactgggct aaatctactg tttcaaaaaa gtgtctttac aaaaaaaca 2850
aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900
caaaaa 2906

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Met  Leu Asn Lys Met Thr Leu His Pro Gln Gln Ile Met Ile Gly
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 20      25      30
Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
 35      40      45
Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
 50      55      60
Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
 65      70      75
Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
 80      85      90
Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
 95     100     105
Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
110     115     120
Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
125     130     135
Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
140     145     150
Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser
155     160     165
Tyr Ala Phe Asn Arg Ile Pro Ser Leu Arg Arg Leu Asp Leu Gly
170     175     180
Glu Leu Lys Arg Leu Ser Tyr Ile Ser Glu Gly Ala Phe Glu Gly
185     190     195
Leu Ser Asn Leu Arg Tyr Leu Asn Leu Ala Met Cys Asn Leu Arg
200     205     210
Glu Ile Pro Asn Leu Thr Pro Leu Ile Lys Leu Asp Glu Leu Asp
215     220     225
Leu Ser Gly Asn His Leu Ser Ala Ile Arg Pro Gly Ser Phe Gln
230     235     240
Gly Leu Met His Leu Gln Lys Leu Trp Met Ile Gln Ser Gln Ile
245     250     255
Gln Val Ile Glu Arg Asn Ala Phe Asp Asn Leu Gln Ser Leu Val
260     265     270
Glu Ile Asn Leu Ala His Asn Asn Leu Thr Leu Leu Pro His Asp
275     280     285
Leu Phe Thr Pro Leu His His Leu Glu Arg Ile His Leu His His

```

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
290 295 300

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Pro | Trp | Asn | Cys | Asn | Cys | Asp | Ile | Leu | Trp | Leu | Ser | Trp | Trp |
| | | | | 305 | | | | | 310 | | | | | 315 |
| Ile | Lys | Asp | Met | Ala | Pro | Ser | Asn | Thr | Ala | Cys | Cys | Ala | Arg | Cys |
| | | | | 320 | | | | | 325 | | | | | 330 |
| Asn | Thr | Pro | Pro | Asn | Leu | Lys | Gly | Arg | Tyr | Ile | Gly | Glu | Leu | Asp |
| | | | | 335 | | | | | 340 | | | | | 345 |
| Gln | Asn | Tyr | Phe | Thr | Cys | Tyr | Ala | Pro | Val | Ile | Val | Glu | Pro | Pro |
| | | | | 350 | | | | | 355 | | | | | 360 |
| Ala | Asp | Leu | Asn | Val | Thr | Glu | Gly | Met | Ala | Ala | Glu | Leu | Lys | Cys |
| | | | | 365 | | | | | 370 | | | | | 375 |
| Arg | Ala | Ser | Thr | Ser | Leu | Thr | Ser | Val | Ser | Trp | Ile | Thr | Pro | Asn |
| | | | | 380 | | | | | 385 | | | | | 390 |
| Gly | Thr | Val | Met | Thr | His | Gly | Ala | Tyr | Lys | Val | Arg | Ile | Ala | Val |
| | | | | 395 | | | | | 400 | | | | | 405 |
| Leu | Ser | Asp | Gly | Thr | Leu | Asn | Phe | Thr | Asn | Val | Thr | Val | Gln | Asp |
| | | | | 410 | | | | | 415 | | | | | 420 |
| Thr | Gly | Met | Tyr | Thr | Cys | Met | Val | Ser | Asn | Ser | Val | Gly | Asn | Thr |
| | | | | 425 | | | | | 430 | | | | | 435 |
| Thr | Ala | Ser | Ala | Thr | Leu | Asn | Val | Thr | Ala | Ala | Thr | Thr | Thr | Pro |
| | | | | 440 | | | | | 445 | | | | | 450 |
| Phe | Ser | Tyr | Phe | Ser | Thr | Val | Thr | Val | Glu | Thr | Met | Glu | Pro | Ser |
| | | | | 455 | | | | | 460 | | | | | 465 |
| Gln | Asp | Glu | Ala | Arg | Thr | Thr | Asp | Asn | Asn | Val | Gly | Pro | Thr | Pro |
| | | | | 470 | | | | | 475 | | | | | 480 |
| Val | Val | Asp | Trp | Glu | Thr | Thr | Asn | Val | Thr | Thr | Ser | Leu | Thr | Pro |
| | | | | 485 | | | | | 490 | | | | | 495 |
| Gln | Ser | Thr | Arg | Ser | Thr | Glu | Lys | Thr | Phe | Thr | Ile | Pro | Val | Thr |
| | | | | 500 | | | | | 505 | | | | | 510 |
| Asp | Ile | Asn | Ser | Gly | Ile | Pro | Gly | Ile | Asp | Glu | Val | Met | Lys | Thr |
| | | | | 515 | | | | | 520 | | | | | 525 |
| Thr | Lys | Ile | Ile | Ile | Gly | Cys | Phe | Val | Ala | Ile | Thr | Leu | Met | Ala |
| | | | | 530 | | | | | 535 | | | | | 540 |
| Ala | Val | Met | Leu | Val | Ile | Phe | Tyr | Lys | Met | Arg | Lys | Gln | His | His |
| | | | | 545 | | | | | 550 | | | | | 555 |
| Arg | Gln | Asn | His | His | Ala | Pro | Thr | Arg | Thr | Val | Glu | Ile | Ile | Asn |
| | | | | 560 | | | | | 565 | | | | | 570 |
| Val | Asp | Asp | Glu | Ile | Thr | Gly | Asp | Thr | Pro | Met | Glu | Ser | His | Leu |
| | | | | 575 | | | | | 580 | | | | | 585 |
| Pro | Met | Pro | Ala | Ile | Glu | His | Glu | His | Leu | Asn | His | Tyr | Asn | Ser |
| | | | | 590 | | | | | 595 | | | | | 600 |
| Tyr | Lys | Ser | Pro | Phe | Asn | His | Thr | Thr | Thr | Val | Asn | Thr | Ile | Asn |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
605 610 615

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620 625 630

Ser Lys Asp Asn Val Gln Glu Thr Gln Ile
635 640

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<211> 4053
<212> DNA

<213> Homo Sapien

<400> 293
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aagtgaaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350
 aatgaaatct cctggactat tgaagacatg aatggtgctt tctctgggct 1400
 tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450
 ctaaaaaagc cttcactggt ttggatgcat tggagcatct agacctgagt 1500
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | | | | | | | | | | | |
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| Pro | Cys | Pro | Thr | Thr | Cys | Arg | Cys | Leu | Gly | Asp | Leu | Leu | Asp | Cys | |
| | | | | 50 | | | | | 55 | | | | | 60 | |
| Ser | Arg | Lys | Arg | Leu | Ala | Arg | Leu | Pro | Glu | Pro | Leu | Pro | Ser | Trp | |
| | | | | 65 | | | | | 70 | | | | | 75 | |
| Val | Ala | Arg | Leu | Asp | Leu | Ser | His | Asn | Arg | Leu | Ser | Phe | Ile | Lys | |
| | | | | 80 | | | | | 85 | | | | | 90 | |
| Ala | Ser | Ser | Met | Ser | His | Leu | Gln | Ser | Leu | Arg | Glu | Val | Lys | Leu | |
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| Asn | Asn | Asn | Glu | Leu | Glu | Thr | Ile | Pro | Asn | Leu | Gly | Pro | Val | Ser | |
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| Ala | Asn | Ile | Thr | Leu | Leu | Ser | Leu | Ala | Gly | Asn | Arg | Ile | Val | Glu | |
| | | | | 125 | | | | | 130 | | | | | 135 | |
| Ile | Leu | Pro | Glu | His | Leu | Lys | Glu | Phe | Gln | Ser | Leu | Glu | Thr | Leu | |
| | | | | 140 | | | | | 145 | | | | | 150 | |
| Asp | Leu | Ser | Ser | Asn | Asn | Ile | Ser | Glu | Leu | Gln | Thr | Ala | Phe | Pro | |
| | | | | 155 | | | | | 160 | | | | | 165 | |
| Ala | Leu | Gln | Leu | Lys | Tyr | Leu | Tyr | Leu | Asn | Ser | Asn | Arg | Val | Thr | |
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| Ser | Met | Glu | Pro | Gly | Tyr | Phe | Asp | Asn | Leu | Ala | Asn | Thr | Leu | Leu | |
| | | | | 185 | | | | | 190 | | | | | 195 | |
| Val | Leu | Lys | Leu | Asn | Arg | Asn | Arg | Ile | Ser | Ala | Ile | Pro | Pro | Lys | |
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| Met | Phe | Lys | Leu | Pro | Gln | Leu | Gln | His | Leu | Glu | Leu | Asn | Arg | Asn | |
| | | | | 215 | | | | | 220 | | | | | 225 | |
| Lys | Ile | Lys | Asn | Val | Asp | Gly | Leu | Thr | Phe | Gln | Gly | Leu | Gly | Ala | |
| | | | | 230 | | | | | 235 | | | | | 240 | |
| Leu | Lys | Ser | Leu | Lys | Met | Gln | Arg | Asn | Gly | Val | Thr | Lys | Leu | Met | |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Asp | Gly | Ala | Phe | Trp | Gly | Leu | Ser | Asn | Met | Glu | Ile | Leu | Gln | Leu | |
| | | | | 260 | | | | | 265 | | | | | 270 | |
| Asp | His | Asn | Asn | Leu | Thr | Glu | Ile | Thr | Lys | Gly | Trp | Leu | Tyr | Gly | |
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| Leu | Asp | Leu | Thr | Phe | Asn | His | Leu | Ser | Arg | Leu | Asp | Asp | Ser | Ser | |
| | | | | 320 | | | | | 325 | | | | | 330 | |
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
 335 340 345

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| Leu Lys Thr Leu | Asp | Leu | Lys | Asn | Asn | Glu | Ile | Ser | Trp | Thr | Ile |
| | 365 | | | | | 370 | | | | | 375 |
| Glu Asp Met Asn | Gly | Ala | Phe | Ser | Gly | Leu | Asp | Lys | Leu | Arg | Arg |
| | 380 | | | | | 385 | | | | | 390 |
| Leu Ile Leu Gln | Gly | Asn | Arg | Ile | Arg | Ser | Ile | Thr | Lys | Lys | Ala |
| | 395 | | | | | 400 | | | | | 405 |
| Phe Thr Gly Leu | Asp | Ala | Leu | Glu | His | Leu | Asp | Leu | Ser | Asp | Asn |
| | 410 | | | | | 415 | | | | | 420 |
| Ala Ile Met Ser | Leu | Gln | Gly | Asn | Ala | Phe | Ser | Gln | Met | Lys | Lys |
| | 425 | | | | | 430 | | | | | 435 |
| Leu Gln Gln Leu | His | Leu | Asn | Thr | Ser | Ser | Leu | Leu | Cys | Asp | Cys |
| | 440 | | | | | 445 | | | | | 450 |
| Gln Leu Lys Trp | Leu | Pro | Gln | Trp | Val | Ala | Glu | Asn | Asn | Phe | Gln |
| | 455 | | | | | 460 | | | | | 465 |
| Ser Phe Val Asn | Ala | Ser | Cys | Ala | His | Pro | Gln | Leu | Leu | Lys | Gly |
| | 470 | | | | | 475 | | | | | 480 |
| Arg Ser Ile Phe | Ala | Val | Ser | Pro | Asp | Gly | Phe | Val | Cys | Asp | Asp |
| | 485 | | | | | 490 | | | | | 495 |
| Phe Pro Lys Pro | Gln | Ile | Thr | Val | Gln | Pro | Glu | Thr | Gln | Ser | Ala |
| | 500 | | | | | 505 | | | | | 510 |
| Ile Lys Gly Ser | Asn | Leu | Ser | Phe | Ile | Cys | Ser | Ala | Ala | Ser | Ser |
| | 515 | | | | | 520 | | | | | 525 |
| Ser Asp Ser Pro | Met | Thr | Phe | Ala | Trp | Lys | Lys | Asp | Asn | Glu | Leu |
| | 530 | | | | | 535 | | | | | 540 |
| Leu His Asp Ala | Glu | Met | Glu | Asn | Tyr | Ala | His | Leu | Arg | Ala | Gln |
| | 545 | | | | | 550 | | | | | 555 |
| Gly Gly Glu Val | Met | Glu | Tyr | Thr | Thr | Ile | Leu | Arg | Leu | Arg | Glu |
| | 560 | | | | | 565 | | | | | 570 |
| Val Glu Phe Ala | Ser | Glu | Gly | Lys | Tyr | Gln | Cys | Val | Ile | Ser | Asn |
| | 575 | | | | | 580 | | | | | 585 |
| His Phe Gly Ser | Ser | Tyr | Ser | Val | Lys | Ala | Lys | Leu | Thr | Val | Asn |
| | 590 | | | | | 595 | | | | | 600 |
| Met Leu Pro Ser | Phe | Thr | Lys | Thr | Pro | Met | Asp | Leu | Thr | Ile | Arg |
| | 605 | | | | | 610 | | | | | 615 |
| Ala Gly Ala Met | Ala | Arg | Leu | Glu | Cys | Ala | Ala | Val | Gly | His | Pro |
| | 620 | | | | | 625 | | | | | 630 |
| Ala Pro Gln Ile | Ala | Trp | Gln | Lys | Asp | Gly | Gly | Thr | Asp | Phe | Pro |
| | 635 | | | | | 640 | | | | | 645 |
| Ala Ala Arg Glu | Arg | Arg | Met | His | Val | Met | Pro | Glu | Asp | Asp | Val |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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| Leu Thr Val Leu | Glu 680 | Thr Pro Ser Phe | Leu 685 | Arg Pro Leu Leu | Asp 690 |
| Arg Thr Val Thr | Lys 695 | Gly Glu Thr Ala | Val 700 | Leu Gln Cys Ile | Ala 705 |
| Gly Gly Ser Pro | Pro 710 | Pro Lys Leu Asn | Trp 715 | Thr Lys Asp Asp | Ser 720 |
| Pro Leu Val Val | Thr 725 | Glu Arg His Phe | Phe 730 | Ala Ala Gly Asn | Gln 735 |
| Leu Leu Ile Ile | Val 740 | Asp Ser Asp Val | Ser 745 | Asp Ala Gly Lys | Tyr 750 |
| Thr Cys Glu Met | Ser 755 | Asn Thr Leu Gly | Thr 760 | Glu Arg Gly Asn | Val 765 |
| Arg Leu Ser Val | Ile 770 | Pro Thr Pro Thr | Cys 775 | Asp Ser Pro Gln | Met 780 |
| Thr Ala Pro Ser | Leu 785 | Asp Asp Asp Gly | Trp 790 | Ala Thr Val Gly | Val 795 |
| Val Ile Ile Ala | Val 800 | Val Cys Cys Val | Val 805 | Gly Thr Ser Leu | Val 810 |
| Trp Val Val Ile | Ile 815 | Tyr His Thr Arg | Arg 820 | Arg Asn Glu Asp | Cys 825 |
| Ser Ile Thr Asn | Thr 830 | Asp Glu Thr Asn | Leu 835 | Pro Ala Asp Ile | Pro 840 |
| Ser Tyr Leu Ser | Ser 845 | Gln Gly Thr Leu | Ala 850 | Asp Arg Gln Asp | Gly 855 |
| Tyr Val Ser Ser | Glu 860 | Ser Gly Ser His | His 865 | Gln Phe Val Thr | Ser 870 |
| Ser Gly Ala Gly | Phe 875 | Phe Leu Pro Gln | His 880 | Asp Ser Ser Gly | Thr 885 |
| Cys His Ile Asp | Asn 890 | Ser Ser Glu Ala | Asp 895 | Val Glu Ala Ala | Thr 900 |
| Asp Leu Phe Leu | Cys 905 | Pro Phe Leu Gly | Ser 910 | Thr Gly Pro Met | Tyr 915 |
| Leu Lys Gly Asn | Val 920 | Tyr Gly Ser Asp | Pro 925 | Phe Glu Thr Tyr | His 930 |
| Thr Gly Cys Ser | Pro 935 | Asp Pro Arg Thr | Val 940 | Leu Met Asp His | Tyr 945 |
| Glu Pro Ser Tyr | Ile 950 | Lys Lys Lys Glu | Cys 955 | Tyr Pro Cys Ser | His 960 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 995 1000 1005
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 Asp Phe Ser Ala Asn Pro Glu Pro Ala Ser Val Ala Ser Ser Asn
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 <213> Artificial Sequence

<220>
 <223> Synthetic Oligonucleotide Probe

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<210> 314
 <211> 3003
 <212> DNA
 <213> Homo Sapien

<400> 314
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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caacctgttc ctgcgcgcc actgcgctgc gccccaggac ccgctgcca 200
acatggattt tctcctggcg ctggtgctgg taccctcgct ctacctgcag 250
gcggccgccc agttcgacgg gaggtggccc aggcaaatag tgtcatcgat 300
tggcctatgt cgttatggtg ggaggattga ctgctgctgg ggctgggctc 350
gccagtcttg gggacagtgt cagcctgtgt gccaaaccag atgcaaacat 400
ggtgaatgta tcggggccaaa caagtgaag tgtcatcctg gttatgctgg 450
aaaaacctgt aatcaagatc taaatgagtg tggcctgaag ccccgccct 500
gtaagcacag gtgcatgaac acttacggca gctacaagtg ctactgtctc 550
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gaatgtcac ttggtcagta tcagtgcagc agctttgctc gatgttataa 900
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 <212> PRT
 <213> Homo Sapien

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 35          40          45
Trp Gly Trp Ala Arg Gln Ser Trp Gly Gln Cys Gln Pro Val Cys
 50          55          60
Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
 65          70          75
Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
 80          85          90
Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
 95          100          105
Asn Thr Tyr Gly Ser Tyr Lys Cys Tyr Cys Leu Asn Gly Tyr Met
 110          115          120
Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
 125          130          135
Ala Asn Cys Gln Tyr Gly Cys Asp Val Val Lys Gly Gln Ile Arg
 140          145          150
Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
 155          160          165
Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
 170          175          180
Pro Arg Phe Arg Gln Cys Val Asn Thr Phe Gly Ser Tyr Ile Cys
 185          190          195
Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
 200          205          210
Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
 215          220          225
Ser Ser Phe Ala Arg Cys Tyr Asn Val Arg Gly Ser Tyr Lys Cys
 230          235          240
Lys Cys Lys Glu Gly Tyr Gln Gly Asp Gly Leu Thr Cys Val Tyr
 245          250          255
Ile Pro Lys Val Met Ile Glu Pro Ser Gly Pro Ile His Val Pro
 260          265          270
Lys Gly Asn Gly Thr Ile Leu Lys Gly Asp Thr Gly Asn Asn Asn
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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|-----------------|---------------------|---------------------|-----|
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| 320 | | 325 | 330 |
| Pro Pro Pro Leu | Pro Thr Glu Leu Arg | Thr Pro Leu Pro Pro | Thr |
| 335 | | 340 | 345 |
| Thr Pro Glu Arg | Pro Thr Thr Gly Leu | Thr Thr Ile Ala Pro | Ala |
| 350 | | 355 | 360 |
| Ala Ser Thr Pro | Pro Gly Gly Ile Thr | Val Asp Asn Arg Val | Gln |
| 365 | | 370 | 375 |
| Thr Asp Pro Gln | Lys Pro Arg Gly Asp | Val Phe Ser Val Leu | Val |
| 380 | | 385 | 390 |
| His Ser Cys Asn | Phe Asp His Gly Leu | Cys Gly Trp Ile Arg | Glu |
| 395 | | 400 | 405 |
| Lys Asp Asn Asp | Leu His Trp Glu Pro | Ile Arg Asp Pro Ala | Gly |
| 410 | | 415 | 420 |
| Gly Gln Tyr Leu | Thr Val Ser Ala Ala | Lys Ala Pro Gly Gly | Lys |
| 425 | | 430 | 435 |
| Ala Ala Arg Leu | Val Leu Pro Leu Gly | Arg Leu Met His Ser | Gly |
| 440 | | 445 | 450 |
| Asp Leu Cys Leu | Ser Phe Arg His Lys | Val Thr Gly Leu His | Ser |
| 455 | | 460 | 465 |
| Gly Thr Leu Gln | Val Phe Val Arg Lys | His Gly Ala His Gly | Ala |
| 470 | | 475 | 480 |
| Ala Leu Trp Gly | Arg Asn Gly Gly His | Gly Trp Arg Gln Thr | Gln |
| 485 | | 490 | 495 |
| Ile Thr Leu Arg | Gly Ala Asp Ile Lys | Ser Glu Ser Gln Arg | |
| 500 | | 505 | |

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<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

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<210> 317

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 317

ttgcacttgt aggaccacg tacg 24

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<210> 318

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 318

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<210> 319

<211> 2110

<212> DNA

<213> Homo Sapien

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 caacaggtgc ttgctcgggg ctgaaggatga cagtgccatc acacactgtc 150
 catggcgtca gaggtcaggc cctctaccta cccgtccact atggcttcca 200
 cactccagca tcagacatcc agatcatatg gctatttgag agaccccaca 250
 caatgcccac atacttactg ggctctgtga ataagtctgt ggttcctgac 300
 ttggaatacc aacacaagtt caccatgatg ccaccaatg catctctgct 350
 tatcaacca ctgcagttcc ctgatgaagg caattacatc gtgaagggtca 400
 acattcaggg aaatggaact ctatctgcca gtcagaagat acaagtcacg 450
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 ggctgtggag tatgtgggga acatgaccct gacatgccat gtggaagggg 550
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 agtaaccaag gaagacattg ggaattacag ctgcctgggtg aggaaccctg 700
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<210> 320
<211> 450
<212> PRT
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20 25 30
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35 40 45
His Thr Pro Ala Ser Asp Ile Gln Ile Ile Trp Leu Phe Glu Arg
50 55 60
Pro His Thr Met Pro Lys Tyr Leu Leu Gly Ser Val Asn Lys Ser
65 70 75
Val Val Pro Asp Leu Glu Tyr Gln His Lys Phe Thr Met Met Pro
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

80

85

90

Pro Asn Ala Ser Leu₉₅ Leu Ile Asn Pro Leu₁₀₀ Gln Phe Pro Asp Glu₁₀₅
 Gly Asn Tyr Ile Val₁₁₀ Lys Val Asn Ile Gln₁₁₅ Gly Asn Gly Thr Leu₁₂₀
 Ser Ala Ser Gln Lys₁₂₅ Ile Gln Val Thr Val₁₃₀ Asp Asp Pro Val Thr₁₃₅
 Lys Pro Val Val Gln₁₄₀ Ile His Pro Pro Ser₁₄₅ Gly Ala Val Glu Tyr₁₅₀
 Val Gly Asn Met Thr₁₅₅ Leu Thr Cys His Val₁₆₀ Glu Gly Gly Thr Arg₁₆₅
 Leu Ala Tyr Gln Trp₁₇₀ Leu Lys Asn Gly Arg₁₇₅ Pro Val His Thr Ser₁₈₀
 Ser Thr Tyr Ser Phe₁₈₅ Ser Pro Gln Asn Asn₁₉₀ Thr Leu His Ile Ala₁₉₅
 Pro Val Thr Lys Glu₂₀₀ Asp Ile Gly Asn Tyr₂₀₅ Ser Cys Leu Val Arg₂₁₀
 Asn Pro Val Ser Glu₂₁₅ Met Glu Ser Asp Ile₂₂₀ Ile Met Pro Ile Ile₂₂₅
 Tyr Tyr Gly Pro Tyr₂₃₀ Gly Leu Gln Val Asn₂₃₅ Ser Asp Lys Gly Leu₂₄₀
 Lys Val Gly Glu Val₂₄₅ Phe Thr Val Asp Leu₂₅₀ Gly Glu Ala Ile Leu₂₅₅
 Phe Asp Cys Ser Ala₂₆₀ Asp Ser His Pro Pro₂₆₅ Asn Thr Tyr Ser Trp₂₇₀
 Ile Arg Arg Thr Asp₂₇₅ Asn Thr Thr Tyr Ile₂₈₀ Ile Lys His Gly Pro₂₈₅
 Arg Leu Glu Val Ala₂₉₀ Ser Glu Lys Val Ala₂₉₅ Gln Lys Thr Met Asp₃₀₀
 Tyr Val Cys Cys Ala₃₀₅ Tyr Asn Asn Ile Thr₃₁₀ Gly Arg Gln Asp Glu₃₁₅
 Thr His Phe Thr Val₃₂₀ Ile Ile Thr Ser Val₃₂₅ Gly Leu Glu Lys Leu₃₃₀
 Ala Gln Lys Gly Lys₃₃₅ Ser Leu Ser Pro Leu₃₄₀ Ala Ser Ile Thr Gly₃₄₅
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 Lys Lys Tyr Gln Pro₃₆₅ Tyr Lys Val Ile Lys₃₇₀ Gln Lys Leu Glu Gly₃₇₅
 Arg Pro Glu Thr Glu₃₈₀ Tyr Arg Lys Ala Gln₃₈₅ Thr Phe Ser Gly His₃₉₀
 Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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410 415 420

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425 430 435

Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His Pro Glu
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<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 321

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<210> 322

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<223> Synthetic Oligonucleotide Probe

<400> 322

cactgacagg gttcctcacc cagg 24

<210> 323

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 323

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<210> 324

<211> 2397

<212> DNA

<213> Homo Sapien

<400> 324

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acgttcgcgt catcacggac gagaactgga gagaactgct ggaaggagac 150

tggatgatag aatttttatgc cccgtggtgc cctgcttgct aaaatcttca 200

accggaatgg gaaagttttg ctgaatgggg agaagatctt gaggttaata 250

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<210> 325

<211> 280

<212> PRT

<213> Homo Sapien

<400> 325

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| Met | Ala | Pro | Ser | Gly | Ser | Leu | Ala | Val | Pro | Leu | Ala | Val | Leu | Val | 1 | 5 | 10 | 15 |
| Leu | Leu | Leu | Trp | Gly | Ala | Pro | Trp | Thr | His | Gly | Arg | Arg | Ser | Asn | 20 | 25 | 30 | |
| Val | Arg | Val | Ile | Thr | Asp | Glu | Asn | Trp | Arg | Glu | Leu | Leu | Glu | Gly | 35 | 40 | 45 | |
| Asp | Trp | Met | Ile | Glu | Phe | Tyr | Ala | Pro | Trp | Cys | Pro | Ala | Cys | Gln | 50 | 55 | 60 | |
| Asn | Leu | Gln | Pro | Glu | Trp | Glu | Ser | Phe | Ala | Glu | Trp | Gly | Glu | Asp | 65 | 70 | 75 | |
| Leu | Glu | Val | Asn | Ile | Ala | Lys | Val | Asp | Val | Thr | Glu | Gln | Pro | Gly | 80 | 85 | 90 | |
| Leu | Ser | Gly | Arg | Phe | Ile | Ile | Thr | Ala | Leu | Pro | Thr | Ile | Tyr | His | 95 | 100 | 105 | |
| Cys | Lys | Asp | Gly | Glu | Phe | Arg | Arg | Tyr | Gln | Gly | Pro | Arg | Thr | Lys | 110 | 115 | 120 | |
| Lys | Asp | Phe | Ile | Asn | Phe | Ile | Ser | Asp | Lys | Glu | Trp | Lys | Ser | Ile | 125 | 130 | 135 | |
| Glu | Pro | Val | Ser | Ser | Trp | Phe | Gly | Pro | Gly | Ser | Val | Leu | Met | Ser | 140 | 145 | 150 | |
| Ser | Met | Ser | Ala | Leu | Phe | Gln | Leu | Ser | Met | Trp | Ile | Arg | Thr | Cys | 155 | 160 | 165 | |
| His | Asn | Tyr | Phe | Ile | Glu | Asp | Leu | Gly | Leu | Pro | Val | Trp | Gly | Ser | 170 | 175 | 180 | |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu
185 190 195
Gly Leu Cys Met Ile Phe Val Ala Asp Cys Leu Cys Pro Ser Lys
200 205 210
Arg Arg Arg Pro Gln Pro Tyr Pro Tyr Pro Ser Lys Lys Leu Leu
215 220 225
Ser Glu Ser Ala Gln Pro Leu Lys Lys Val Glu Glu Glu Gln Glu
230 235 240
Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
245 250 255
Gly Thr Asn Lys Asp Phe Pro Gln Asn Ala Ile Arg Gln Arg Ser
260 265 270
Leu Gly Pro Ser Leu Ala Thr Asp Lys Ser
275 280

<210> 326
<211> 23
<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 326
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<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 327
tatgtggatc aggacgtgcc 20

<210> 328
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 328
tgcagggttc agtctagatt g 21

<210> 329
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 329
ttgaaggaca aaggcaatct gccac 25

<210> 330

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 330
ggagtcttgc agttcccctg gcagtcctgg tgctgttgct ttggg 45

<210> 331

<211> 2168

<212> DNA

<213> Homo Sapien

<400> 331
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aacgggaccc ttctgtgtgc cagaaaccgc aagcagttgc taaccagtg 100
ggacaggcgg attggaagag cgggaaggct ctggcccaga gcagtgtgac 150
acttccctct gtgaccatga aactctgggt gtctgcattg ctgatggcct 200
ggtttggtgt cctgagctgt gtgcaggccg aattcttcac ctctattggg 250
cacatgactg acctgattta tgcagagaaa gagctggtgc agtctctgaa 300
agagtacatc cttgtggagg aagccaagct ttccaagatt aagagctggg 350
ccaacaaaat ggaagccttg actagcaagt cagctgctga tgctgagggc 400
tacctggctc accctgtgaa tgcctacaaa ctggtgaagc ggctaaacac 450
agactggcct gcgctggagg acctgtcct gcaggactca gctgcaggtt 500
ttatcgccaa cctctctgtg cagcggcagt tcttccccac tgatgaggac 550
gagataggag ctgccaaagc cctgatgaga cttcaggaca catacaggct 600
ggaccaggc acaatttcca gaggggaact tccaggaacc aagtaccagg 650
caatgctgag tgtggatgac tgctttggga tgggccgctc ggcctacaat 700
gaaggggact attatcatalc ggtgttgttg atggagcagg tgctaaagca 750
gcttgatgcc ggggaggagg ccaccacaac caagtcacag gtgctggact 800
acctcagcta tgctgtcttc cagttgggtg atctgcaccg tgccctggag 850
ctcaccgcc gcctgtctc cttgaccca agccacgaac gagctggagg 900
gaatctgcgg tactttgagc agttattgga ggaagagaga gaaaaaacgt 950
taacaaatca gacagaagct gagctagcaa cccagaagg catctatgag 1000
aggcctgtgg actacctgcc tgagagggat gtttacgaga gcctctgtcg 1050

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

tggggagggt gtcaaaactga caccgccgtag acagaagagg cttttctgta 1100
 ggtaccacca tggcaacagg gccccacagc tgctcattgc ccccttcaaa 1150
 gaggaggacg agtgggacag cccgcacatc gtcaggtact acgatgtcat 1200
 gtctgatgag gaaatcgaga ggatcaagga gatcgcaaaa cctaaacttg 1250
 cacgagccac cgttcgtgat cccaagacag gagtcctcac tgtcgccagc 1300
 taccggggttt ccaaaaagctc ctggctagag gaagatgatg accctgttgt 1350
 ggcccagta aatcgtcggg tgcagcatat cacagggtta acagtaaaga 1400
 ctgcagaatt gttacagggt gcaaattatg gagtgggagg acagtatgaa 1450
 ccgcacttcg acttctctag gcgacctttt gacagcggcc tcaaaacaga 1500
 ggggaatagg ttagcgacgt ttcttaacta catgagtgat gtagaagctg 1550
 gtggtgccac cgtcttccct gatctggggg ctgcaatttg gcctaagaag 1600
 ggtacagctg tgttctggta caacctcttg cggagcgggg aagggtgacta 1650
 ccgaacaaga catgctgcct gccctgtgct tgtgggctgc aagtgggtct 1700
 ccaataagtg gttccatgaa cgaggacagg agttcttgag acctgtgga 1750
 tcaacagaag ttgactgaca tccttttctg tccttcccct tcctggctct 1800
 tcagcccatg tcaacgtgac agacacctt gtatgttcct ttgtatgttc 1850
 ctatcaggct gatttttgga gaaatgaatg tttgtctgga gcagaggag 1900
 accatactag ggcgactcct gtgtgactga agtcccagcc cttccattca 1950
 gcctgtgcca tccctggccc caaggctagg atcaaagtgg ctgcagcaga 2000
 gttagctgtc tagcgcctag caaggctcct ttgtacctca ggtgttttag 2050
 gtgtgagatg tttcagtga ccaaagtctt gataccttgt ttacatgttt 2100
 gtttttatgg catttctatc tattgtggct ttacaaaaa ataaaatgtc 2150
 cctaccagaa aaaaaaaaa 2168

<210> 332
 <211> 533
 <212> PRT
 <213> Homo Sapien

<400> 332
 Met Lys Leu Trp Val Ser Ala Leu Leu Met Ala Trp Phe Gly Val
 1 5 10 15
 Leu Ser Cys Val Gln Ala Glu Phe Phe Thr Ser Ile Gly His Met
 20 25 30
 Thr Asp Leu Ile Tyr Ala Glu Lys Glu Leu Val Gln Ser Leu Lys
 35 40 45
 Glu Tyr Ile Leu Val Glu Glu Ala Lys Leu Ser Lys Ile Lys Ser
 50 55 60

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Trp | Ala | Asn | Lys | Met | Glu | Ala | Leu | Thr | Ser | Lys | Ser | Ala | Ala | Asp | 65 | 70 | 75 |
| Ala | Glu | Gly | Tyr | Leu | Ala | His | Pro | Val | Asn | Ala | Tyr | Lys | Leu | Val | 80 | 85 | 90 |
| Lys | Arg | Leu | Asn | Thr | Asp | Trp | Pro | Ala | Leu | Glu | Asp | Leu | Val | Leu | 95 | 100 | 105 |
| Gln | Asp | Ser | Ala | Ala | Gly | Phe | Ile | Ala | Asn | Leu | Ser | Val | Gln | Arg | 110 | 115 | 120 |
| Gln | Phe | Phe | Pro | Thr | Asp | Glu | Asp | Glu | Ile | Gly | Ala | Ala | Lys | Ala | 125 | 130 | 135 |
| Leu | Met | Arg | Leu | Gln | Asp | Thr | Tyr | Arg | Leu | Asp | Pro | Gly | Thr | Ile | 140 | 145 | 150 |
| Ser | Arg | Gly | Glu | Leu | Pro | Gly | Thr | Lys | Tyr | Gln | Ala | Met | Leu | Ser | 155 | 160 | 165 |
| Val | Asp | Asp | Cys | Phe | Gly | Met | Gly | Arg | Ser | Ala | Tyr | Asn | Glu | Gly | 170 | 175 | 180 |
| Asp | Tyr | Tyr | His | Thr | Val | Leu | Trp | Met | Glu | Gln | Val | Leu | Lys | Gln | 185 | 190 | 195 |
| Leu | Asp | Ala | Gly | Glu | Glu | Ala | Thr | Thr | Thr | Lys | Ser | Gln | Val | Leu | 200 | 205 | 210 |
| Asp | Tyr | Leu | Ser | Tyr | Ala | Val | Phe | Gln | Leu | Gly | Asp | Leu | His | Arg | 215 | 220 | 225 |
| Ala | Leu | Glu | Leu | Thr | Arg | Arg | Leu | Leu | Ser | Leu | Asp | Pro | Ser | His | 230 | 235 | 240 |
| Glu | Arg | Ala | Gly | Gly | Asn | Leu | Arg | Tyr | Phe | Glu | Gln | Leu | Leu | Glu | 245 | 250 | 255 |
| Glu | Glu | Arg | Glu | Lys | Thr | Leu | Thr | Asn | Gln | Thr | Glu | Ala | Glu | Leu | 260 | 265 | 270 |
| Ala | Thr | Pro | Glu | Gly | Ile | Tyr | Glu | Arg | Pro | Val | Asp | Tyr | Leu | Pro | 275 | 280 | 285 |
| Glu | Arg | Asp | Val | Tyr | Glu | Ser | Leu | Cys | Arg | Gly | Glu | Gly | Val | Lys | 290 | 295 | 300 |
| Leu | Thr | Pro | Arg | Arg | Gln | Lys | Arg | Leu | Phe | Cys | Arg | Tyr | His | His | 305 | 310 | 315 |
| Gly | Asn | Arg | Ala | Pro | Gln | Leu | Leu | Ile | Ala | Pro | Phe | Lys | Glu | Glu | 320 | 325 | 330 |
| Asp | Glu | Trp | Asp | Ser | Pro | His | Ile | Val | Arg | Tyr | Tyr | Asp | Val | Met | 335 | 340 | 345 |
| Ser | Asp | Glu | Glu | Ile | Glu | Arg | Ile | Lys | Glu | Ile | Ala | Lys | Pro | Lys | 350 | 355 | 360 |
| Leu | Ala | Arg | Ala | Thr | Val | Arg | Asp | Pro | Lys | Thr | Gly | Val | Leu | Thr | 365 | 370 | 375 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Ala | Ser | Tyr | Arg | Val | Ser | Lys | Ser | Ser | Trp | Leu | Glu | Glu | Asp |
| | | | | 380 | | | | | 385 | | | | | 390 |
| Asp | Asp | Pro | Val | Val | Ala | Arg | Val | Asn | Arg | Arg | Met | Gln | His | Ile |
| | | | | 395 | | | | | 400 | | | | | 405 |
| Thr | Gly | Leu | Thr | Val | Lys | Thr | Ala | Glu | Leu | Leu | Gln | Val | Ala | Asn |
| | | | | 410 | | | | | 415 | | | | | 420 |
| Tyr | Gly | Val | Gly | Gly | Gln | Tyr | Glu | Pro | His | Phe | Asp | Phe | Ser | Arg |
| | | | | 425 | | | | | 430 | | | | | 435 |
| Arg | Pro | Phe | Asp | Ser | Gly | Leu | Lys | Thr | Glu | Gly | Asn | Arg | Leu | Ala |
| | | | | 440 | | | | | 445 | | | | | 450 |
| Thr | Phe | Leu | Asn | Tyr | Met | Ser | Asp | Val | Glu | Ala | Gly | Gly | Ala | Thr |
| | | | | 455 | | | | | 460 | | | | | 465 |
| Val | Phe | Pro | Asp | Leu | Gly | Ala | Ala | Ile | Trp | Pro | Lys | Lys | Gly | Thr |
| | | | | 470 | | | | | 475 | | | | | 480 |
| Ala | Val | Phe | Trp | Tyr | Asn | Leu | Leu | Arg | Ser | Gly | Glu | Gly | Asp | Tyr |
| | | | | 485 | | | | | 490 | | | | | 495 |
| Arg | Thr | Arg | His | Ala | Ala | Cys | Pro | Val | Leu | Val | Gly | Cys | Lys | Trp |
| | | | | 500 | | | | | 505 | | | | | 510 |
| Val | Ser | Asn | Lys | Trp | Phe | His | Glu | Arg | Gly | Gln | Glu | Phe | Leu | Arg |
| | | | | 515 | | | | | 520 | | | | | 525 |
| Pro | Cys | Gly | Ser | Thr | Glu | Val | Asp | | | | | | | |
| | | | | 530 | | | | | | | | | | |

<210> 333

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 333

ccaggcaciaa tttccaga 18

<210> 334

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 334

ggacccttct gtgtgccag 19

<210> 335

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<400> 335
ggtctcaaga actcctgtc 19

<210> 336
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 336
acactcagca ttgcctggta cttg 24

<210> 337
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Oligonucleotide Probe

<400> 337
gggcacatga ctgacctgat ttatgcagag aaagagctgg tgcag 45

<210> 338
<211> 2789

<212> DNA
<213> Homo Sapien

<400> 338
gcagtattga gttttacttc ctctctttt tagtgggaaga cagaccataa 50
tcccagtgtg agtgaaattg attgtttcat ttattaccgt tttggctggg 100
ggtagtttcc gacaccttca cagttgaaga gcaggcagaa ggagttgtga 150
agacaggaca atcttcttgg ggatgctggt cctggaagcc agcgggcctt 200
gctctgtctt tggcctcatt gaccccaggt tctctgggta aaactgaaag 250
cctactactg gcctgggtgcc catcaatcca ttgatccttg aggctgtgcc 300
cctggggcac ccacctggca gggcctacca ccatgcgact gagctccctg 350
ttggctctgc tgcggccagc gcttccccctc atcttagggc tgtctctggg 400
gtgcagcctg agcctcctgc gggtttcctg gatccagggg gagggagaag 450
atccctgtgt cgaggctgta ggggagcgag gagggccaca gaatccagat 500
tcgagagctc ggctagacca aagtgatgaa gacttcaaac cccggattgt 550
cccctactac agggacccca acaagcccta caagaagggtg ctcaggactc 600
ggtacatcca gacagagctg ggctcccgtg agcggttgct ggtggctgtc 650
ctgacctccc gagctacact gtccactttg gccgtggctg tgaaccgtac 700
ggtggcccat cacttccctc ggttactcta cttcactggg cagcgggggg 750

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cccgggctcc agcagggatg cagggtggtg ctcattgggga tgagcggccc 800
gcctggctca tgtcagagac cctgcgccac cttcacacac actttggggc 850
cgactacgac tggttcttca tcatgcagga tgacacatat gtgcaggccc 900
cccgccctggc agcccttgct ggccacctca gcatcaacca agacctgtac 950
ttaggccggg cagaggagt ctttggcgca ggcgagcagg cccggtactg 1000
tcattggggg tttggctacc tgtgtgcag gagtctcctg cttcgtctgc 1050
ggccacatct ggatggctgc cgaggagaca ttctcagtgc ccgtcctgac 1100
gagtggcttg gacgctgcct cattgactct ctgggcgtcg gctgtgtctc 1150
acagcaccag gggcagcagt atcgctcatt tgaactggcc aaaaataggg 1200
accctgagaa ggaagggagc tcggctttcc tgagtgcctt cgccgtgcac 1250
cctgtctccg aaggctaccct catgtaccgg ctccacaaac gcttcagcgc 1300
tctggagttg gagcgggctt acagtgaat agaacaactg caggctcaga 1350
tccggaacct gaccgtgctg acccccgaag gggaggcagg gctgagctgg 1400
cccgttggg tccctgctcc ttccacacca cactctcgct ttgaggtgct 1450
gggctgggac tacttcacag agcagcacac cttctcctgt gcagatgggg 1500
ctcccaagtg ccactacag ggggctagca gggcggacgt gggatgatgcg 1550
ttggagactg ccctggagca gctcaatcgg cgctatcagc cccgcctgcg 1600
cttcagaag cagcgactgc tcaacggcta tcggcgcttc gaccagcac 1650
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agctggtgct gccactcctg gtggctgaag ctgctgcagc cccggctttc 1850
ctcgaggcgt ttgcagcaa tgcctggag ccacgagaac atgcattgct 1900
caccctgttg ctggtctacg ggccacgaga aggtggccgt ggagctccag 1950
accattttct tggggtgaag gctgcagcag cggagttaga gcgacggtag 2000
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tcttccttac caccgtgtgg acaaggcctg ggcccgaagt cctcaaccgc 2150
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ccaggagttc aatcctgccc tgtcaccaca gagatcacc ccaggggccc 2250
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ggggctccta taggggggag atttgaccgg caggcttctg cggagggtg 2350

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

cttctacaac gctgactacc tggcggcccg agccccggctg gcaggtgaac 2400
 tggcaggcca ggaagaggag gaagccctgg aggggctgga ggtgatggat 2450
 gttttcctcc ggttctcagg gctccacctc tttcgggccc tagagccagg 2500
 gctggtgcag aagttctccc tgcgagactg cagcccacgg ctcaagtgaag 2550
 aactctacca ccgctgccgc ctcagcaacc tggaggggct agggggccgt 2600
 gcccagctgg ctatggctct ctttgagcag gagcaggcca atagcactta 2650
 gcccgcctgg gggccctaac ctattacct ttcctttgtc tgcctcagcc 2700
 ccaggaaggg caaggcaaga tgggtggacag atagagaatt gttgctgtat 2750
 tttttaaata tgaaaatggt attaaacatg tcttctgcc 2789

<210> 339
 <211> 772
 <212> PRT
 <213> Homo Sapien

<400> 339
 Met Arg Leu Ser Ser Leu Leu Ala Leu Leu Arg Pro Ala Leu Pro
 1 5 10 15
 Leu Ile Leu Gly Leu Ser Leu Gly Cys Ser Leu Ser Leu Leu Arg
 20 25 30
 Val Ser Trp Ile Gln Gly Glu Gly Glu Asp Pro Cys Val Glu Ala
 35 40 45
 Val Gly Glu Arg Gly Gly Pro Gln Asn Pro Asp Ser Arg Ala Arg
 50 55 60
 Leu Asp Gln Ser Asp Glu Asp Phe Lys Pro Arg Ile Val Pro Tyr
 65 70 75
 Tyr Arg Asp Pro Asn Lys Pro Tyr Lys Lys Val Leu Arg Thr Arg
 80 85 90
 Tyr Ile Gln Thr Glu Leu Gly Ser Arg Glu Arg Leu Leu Val Ala
 95 100 105
 Val Leu Thr Ser Arg Ala Thr Leu Ser Thr Leu Ala Val Ala Val
 110 115 120
 Asn Arg Thr Val Ala His His Phe Pro Arg Leu Leu Tyr Phe Thr
 125 130 135
 Gly Gln Arg Gly Ala Arg Ala Pro Ala Gly Met Gln Val Val Ser
 140 145 150
 His Gly Asp Glu Arg Pro Ala Trp Leu Met Ser Glu Thr Leu Arg
 155 160 165
 His Leu His Thr His Phe Gly Ala Asp Tyr Asp Trp Phe Phe Ile
 170 175 180
 Met Gln Asp Asp Thr Tyr Val Gln Ala Pro Arg Leu Ala Ala Leu
 185 190 195

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

| | | | |
|---------------------|---------------------|---------------------|-----|
| Ala Gly His Leu Ser | Ile Asn Gln Asp | Leu Tyr Leu Gly Arg | Ala |
| 200 | | 205 | 210 |
| Glu Glu Phe Ile Gly | Ala Gly Glu Gln | Ala Arg Tyr Cys His | Gly |
| 215 | | 220 | 225 |
| Gly Phe Gly Tyr Leu | Leu Ser Arg Ser | Leu Leu Leu Arg Leu | Arg |
| 230 | | 235 | 240 |
| Pro His Leu Asp Gly | Cys Arg Gly Asp | Ile Leu Ser Ala Arg | Pro |
| 245 | | 250 | 255 |
| Asp Glu Trp Leu Gly | Arg Cys Leu Ile | Asp Ser Leu Gly Val | Gly |
| 260 | | 265 | 270 |
| Cys Val Ser Gln His | Gln Gly Gln Gln | Tyr Arg Ser Phe Glu | Leu |
| 275 | | 280 | 285 |
| Ala Lys Asn Arg Asp | Pro Glu Lys Glu | Gly Ser Ser Ala Phe | Leu |
| 290 | | 295 | 300 |
| Ser Ala Phe Ala Val | His Pro Val Ser | Glu Gly Thr Leu Met | Tyr |
| 305 | | 310 | 315 |
| Arg Leu His Lys Arg | Phe Ser Ala Leu | Glu Leu Glu Arg Ala | Tyr |
| 320 | | 325 | 330 |
| Ser Glu Ile Glu Gln | Leu Gln Ala Gln | Ile Arg Asn Leu Thr | Val |
| 335 | | 340 | 345 |
| Leu Thr Pro Glu Gly | Glu Ala Gly Leu | Ser Trp Pro Val Gly | Leu |
| 350 | | 355 | 360 |
| Pro Ala Pro Phe Thr | Pro His Ser Arg | Phe Glu Val Leu Gly | Trp |
| 365 | | 370 | 375 |
| Asp Tyr Phe Thr Glu | Gln His Thr Phe | Ser Cys Ala Asp Gly | Ala |
| 380 | | 385 | 390 |
| Pro Lys Cys Pro Leu | Gln Gly Ala Ser | Arg Ala Asp Val Gly | Asp |
| 395 | | 400 | 405 |
| Ala Leu Glu Thr Ala | Leu Glu Gln Leu | Asn Arg Arg Tyr Gln | Pro |
| 410 | | 415 | 420 |
| Arg Leu Arg Phe Gln | Lys Gln Arg Leu | Leu Asn Gly Tyr Arg | Arg |
| 425 | | 430 | 435 |
| Phe Asp Pro Ala Arg | Gly Met Glu Tyr | Thr Leu Asp Leu Leu | Leu |
| 440 | | 445 | 450 |
| Glu Cys Val Thr Gln | Arg Gly His Arg | Arg Ala Leu Ala Arg | Arg |
| 455 | | 460 | 465 |
| Val Ser Leu Leu Arg | Pro Leu Ser Arg | Val Glu Ile Leu Pro | Met |
| 470 | | 475 | 480 |
| Pro Tyr Val Thr Glu | Ala Thr Arg Val | Gln Leu Val Leu Pro | Leu |
| 485 | | 490 | 495 |
| Leu Val Ala Glu Ala | Ala Ala Ala Ala Pro | Ala Phe Leu Glu Ala | Phe |
| 500 | | 505 | 510 |

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

Ala Ala Asn Val Leu Glu Pro Arg Glu His Ala Leu Leu Thr Leu
515 520 525

Leu Leu Val Tyr Gly Pro Arg Glu Gly Gly Arg Gly Ala Pro Asp
530 535 540

Pro Phe Leu Gly Val Lys Ala Ala Ala Ala Glu Leu Glu Arg Arg
545 550 555

Tyr Pro Gly Thr Arg Leu Ala Trp Leu Ala Val Arg Ala Glu Ala
560 565 570

Pro Ser Gln Val Arg Leu Met Asp Val Val Ser Lys Lys His Pro
575 580 585

Val Asp Thr Leu Phe Phe Leu Thr Thr Val Trp Thr Arg Pro Gly
590 595 600

Pro Glu Val Leu Asn Arg Cys Arg Met Asn Ala Ile Ser Gly Trp
605 610 615

Gln Ala Phe Phe Pro Val His Phe Gln Glu Phe Asn Pro Ala Leu
620 625 630

Ser Pro Gln Arg Ser Pro Pro Gly Pro Pro Gly Ala Gly Pro Asp
635 640 645

Pro Pro Ser Pro Pro Gly Ala Asp Pro Ser Arg Gly Ala Pro Ile
650 655 660

Gly Gly Arg Phe Asp Arg Gln Ala Ser Ala Glu Gly Cys Phe Tyr
665 670 675

Asn Ala Asp Tyr Leu Ala Ala Arg Ala Arg Leu Ala Gly Glu Leu
680 685 690

Ala Gly Gln Glu Glu Glu Glu Ala Leu Glu Gly Leu Glu Val Met
695 700 705

Asp Val Phe Leu Arg Phe Ser Gly Leu His Leu Phe Arg Ala Val
710 715 720

Glu Pro Gly Leu Val Gln Lys Phe Ser Leu Arg Asp Cys Ser Pro
725 730 735

Arg Leu Ser Glu Glu Leu Tyr His Arg Cys Arg Leu Ser Asn Leu
740 745 750

Glu Gly Leu Gly Gly Arg Ala Gln Leu Ala Met Ala Leu Phe Glu
755 760 765

Gln Glu Gln Ala Asn Ser Thr
770

<210> 340

<211> 1572

<212> DNA

<213> Homo Sapien

<400> 340

cggagtgggtg cgccaacgtg agaggaaacc cgtgcgcggc tgcgctttcc 50

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
tgtccccaag ccgttctaga cgcgggaaaa atgctttctg aaagcagctc 100

ctttttgaag ggtgtgatgc ttggaagcat tttctgtgct ttgatcacta 150
tgctaggaca cattaggatt ggtcatggaa atagaatgca ccaccatgag 200
catcatcacc tacaagctcc taacaaagaa gatatttga aaatttcaga 250
ggatgagcgc atggagctca gtaagagctt tcgagtatac tgtattatcc 300
ttgtaaaacc caaagatgtg agtctttggg ctgcagtaaa ggagacttgg 350
accaaact gtgacaaagc agagttcttc agttctgaaa atgttaaagt 400
gtttgagtca attaatatgg acacaaatga catgtgggta atgatgagaa 450
aagcttaca atacgccttt gataagtata gagaccaata caactgggtc 500
ttccttgac gccccactac gtttgctatc attgaaaacc taaagtattt 550
tttgttaaaa aaggatccat cacagccttt ctatctaggc cacactataa 600
aatctggaga cttgaatat gtgggtatgg aaggaggaat tgtcttaagt 650
gtagaatcaa tgaaaagact taacagcctt ctcaatatcc cagaaaagt 700
tcctgaacag ggagggatga tttggaagat atctgaagat aaacagctag 750
cagtttgctt gaaatatgct ggagtatttg cagaaaatgc agaagatgct 800
gatggaaaag atgtatttaa taccaaactt gttgggcttt ctattaaaga 850
ggcaatgact tatcacccca accaggtagt agaaggctgt tgttcagata 900
tggtgtttac ttttaatgga ctgactccaa atcagatgca tgtgatgatg 950
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gcaaatgata tctctagttg tgaatttgtg attaaagtaa aacttttagc 1450
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gttccaatgg atttgccttc tcaaaatgta caactaagca actaaagaaa 1550
attaaagtga aagttgaaaa at 1572

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 318

<212> PRT

<213> Homo Sapien

<400> 341

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Gly His Gly Asn Arg Met His His His Glu His His His Leu Gln
          35           40           45
Ala Pro Asn Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg
          50           55           60
Met Glu Leu Ser Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val
          65           70           75
Lys Pro Lys Asp Val Ser Leu Trp Ala Ala Val Lys Glu Thr Trp
          80           85           90
Thr Lys His Cys Asp Lys Ala Glu Phe Phe Ser Ser Glu Asn Val
          95          100          105
Lys Val Phe Glu Ser Ile Asn Met Asp Thr Asn Asp Met Trp Leu
          110          115          120
Met Met Arg Lys Ala Tyr Lys Tyr Ala Phe Asp Lys Tyr Arg Asp
          125          130          135
Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr Thr Phe Ala Ile
          140          145          150
Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp Pro Ser Gln
          155          160          165
Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu Glu Tyr
          170          175          180
Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met Lys
          185          190          195
Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln
          200          205          210
Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val
          215          220          225
Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala
          230          235          240
Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile
          245          250          255
Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys
          260          265          270
Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln
          275          280          285
Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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<211> 18

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<400> 343

ctggttcttc cttgcacg 18

<210> 344

<211> 28

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 344

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<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

<400> 345

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<210> 346

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 346

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 <400> 348
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 <400> 351
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 <210> 352
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<212> DNA
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<220>

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<400> 358

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<210> 359

<211> 48

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<212> DNA

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<210> 363

<211> 48

<212> DNA

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<211> 47

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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 <212> DNA
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 <400> 368
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 <400> 369

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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<211> 48

<212> DNA

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<400> 370

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<400> 371

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<211> 47

<212> DNA

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<210> 373

<211> 48

<212> DNA

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<212> DNA

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<220>

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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 tgctttctctt cccaaatggtt cttatggact gttgctggga tccccatcct 200
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 gaactgggaa tatttttcaat ccagctgcta cttcttttct actgacacca 400
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<210> 377
 <211> 219
 <212> PRT
 <213> Homo Sapien

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 20 25 30

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
 Ile Leu Phe Leu Ser Ala Cys Phe Ile Thr Arg Cys Val Val Thr
 35 40 45

Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro
 50 55 60

Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser
 65 70 75

Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser
 80 85 90

Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu
 95 100 105

Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser
 110 115 120

Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg
 125 130 135

Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp
 140 145 150

Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp
 155 160 165

Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala
 170 175 180

Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val
 185 190 195

Thr Cys Phe Leu Asn Tyr Phe Arg Ile Cys Glu Met Val Gly Ile
 200 205 210

Asn Pro Leu Asn Lys Gly Lys Ser Leu
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<211> 21

<212> DNA

<213> Artificial Sequence

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<223> Synthetic Oligonucleotide Probe

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<210> 379

<211> 24

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<210> 380

<211> 49

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<210> 382
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<220>
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<220>
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<210> 389
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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<223> Synthetic oligonucleotide probe

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<210> 394

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gaagagcaca gctgcagatc c 21

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<213> Artificial Sequence

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<210> 398

<211> 20

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ggcagagact tccagtcact ga 22

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<400> 409
cgatcttctc cacccaggag cgg 23

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<220>
<223> Synthetic oligonucleotide probe

<400> 410
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<211> 23
<212> DNA
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<223> Synthetic oligonucleotide probe

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<210> 412
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<223> Synthetic oligonucleotide probe

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<210> 413
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cagagcagag ggtgccttg 19

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CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

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<223> synthetic oligonucleotide probe

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<220>
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<400> 419
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<210> 420

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt

<211> 23

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<223> Synthetic oligonucleotide probe

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<211> 21

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<223> Synthetic oligonucleotide probe

<400> 421

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<210> 422

<211> 3554

<212> DNA

<213> Homo Sapien

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tcaaatccag caatcgaacc ccagtggtag aggaatttga aagtgtggaa 200
ctgtcttgca tcattacgga ttcgcagaca agtgacccca ggatcgagtg 250
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 ccca 3554

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 <212> PRT
 <213> Homo Sapien

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 20 25 30
 Ala Val Asn Leu Lys Ser Ser Asn Arg Thr Pro Val Val Gln Glu
 35 40 45
 Phe Glu Ser Val Glu Leu Ser Cys Ile Ile Thr Asp Ser Gln Thr
 50 55 60

CORRECTED SEQUENCE LISTING FROM 10466.14 01.29.02P1618P2C1.txt
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Thr Tyr Val Phe Phe Asp Asn Lys Ile Gln Gly Asp Leu Ala Gly
 80 85 90

Arg Ala Glu Ile Leu Gly Lys Thr Ser Leu Lys Ile Trp Asn Val
 95 100 105

Thr Arg Arg Asp Ser Ala Leu Tyr Arg Cys Glu Val Val Ala Arg
 110 115 120

Asn Asp Arg Lys Glu Ile Asp Glu Ile Val Ile Glu Leu Thr Val
 125 130 135

Gln Val Lys Pro Val Thr Pro Val Cys Arg Val Pro Lys Ala Val
 140 145 150

Pro Val Gly Lys Met Ala Thr Leu His Cys Gln Glu Ser Glu Gly
 155 160 165

His Pro Arg Pro His Tyr Ser Trp Tyr Arg Asn Asp Val Pro Leu
 170 175 180

Pro Thr Asp Ser Arg Ala Asn Pro Arg Phe Arg Asn Ser Ser Phe
 185 190 195

His Leu Asn Ser Glu Thr Gly Thr Leu Val Phe Thr Ala Val His
 200 205 210

Lys Asp Asp Ser Gly Gln Tyr Tyr Cys Ile Ala Ser Asn Asp Ala
 215 220 225

Gly Ser Ala Arg Cys Glu Glu Gln Glu Met Glu Val Tyr Asp Leu
 230 235 240

Asn Ile Gly Gly Ile Ile Gly Gly Val Leu Val Val Leu Ala Val
 245 250 255

Leu Ala Leu Ile Thr Leu Gly Ile Cys Cys Ala Tyr Arg Arg Gly
 260 265 270

Tyr Phe Ile Asn Asn Lys Gln Asp Gly Glu Ser Tyr Lys Asn Pro
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Gly Lys Pro Asp Gly Val Asn Tyr Ile Arg Thr Asp Glu Glu Gly
 290 295 300

Asp Phe Arg His Lys Ser Ser Phe Val Ile
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